

2 32  
CGA GTA AAT CGT TCT CGA AGC CTT AGT AAT AGC AAT CCA GAT ATA TCT GGG ACT CCC ACG  
arg val asn arg ser arg ser leu ser asn ser asn pro asp ile ser gly thr pro thr

62 92  
TCA CCA GAT GAT GAA GTT CGA TCA ATC ATC GGG AGT AAG GGT TTA GAT CGC TCC AAT TCC  
ser pro asp asp glu val arg ser ile ile gly ser lys gly leu asp arg ser asn ser

122 152  
TGG GTT AAC ACT GGT GGT CCA AAA GCT GCC CCA TGG GGA TCC AAC CCC AGT CCA AGT GCA  
trp val asn thr gly gly pro lys ala ala pro trp gly ser asn pro ser pro ser ala

182 212  
GAA TCA ACA CAG GCT ATG GAT CGA AGT TGT AAT CGT ATG TCT TCG CAC ACA GAG ACG TCA  
glu ser thr gln ala met asp arg ser cys asn arg met ser ser his thr glu thr ser

242 272  
AGT TTC TTA CAA ACA TTA ACG GGA CGC TTA CCA ACT AAA AAG CTT TTT CAC GAG GAG CTG  
ser phe leu gln thr leu thr gly arg leu pro thr lys lys leu phe his glu glu leu

302 332  
GCT TTG CAG TGG GTT GTT TGC AGT GGC AGC GTT CGG GAA TCA GCT TTG CAA CAA GCC TGG  
ala leu gln trp val val cys ser gly ser val arg glu ser ala leu gln gln ala trp

362 392  
TTC TTT TTT GAA TTA ATG GTA AAG AGC ATG GTG CAC CAT TTA TAC TTT AAT GAT AAA CTT  
phe phe phe glu leu met val lys ser met val his his leu tyr phe asn asp lys leu

Cadherin  
422 |xxx cleavage xx| 452  
GAG GCT CCA AGG AAA AGT CGT TTT CCA GAA CGT TTC ATG GAT GAC ATT GCA GCT CTT GTC  
glu ala pro arg lys ser arg phe pro glu arg phe met asp asp ile ala ala leu val

482 512  
AGC ACG ATT GCT AGT GAT ATA GTT TCA CGA TTT CAG AAG GAC ACA GAA ATG GTT GAG AGA  
ser thr ile ala ser asp ile val ser arg phe gln lys asp thr glu met val glu arg

542 572  
CTC AAT ACA AGC CTT GCA TTC TTT CTC AAT GAT CTG TTG TCT GTT ATG GAC AGA GGA TTT  
leu asn thr ser leu ala phe phe leu asn asp leu leu ser val met asp arg gly phe

602 632  
GTT TTT AGC CTT ATA AAG TCC TGC TAT AAA CAG GTG TCT TCA AAG CTT TAC TCA TTA CCG  
val phe ser leu ile lys ser cys tyr lys gln val ser ser lys leu tyr ser leu pro

662 692  
AAT CCC AGT GTT CTG GTG TCC TTG AGG CTG GAT TTT CTA CGA ATC ATC TGC AGT CAT GAG  
asn pro ser val leu val ser leu arg leu asp phe leu arg ile ile cys ser his glu

722 752  
CAC TAT GTT ACA TTA AAC TTA CCC TGC AGC TTA CTT ACT CCA CCT GCA TCT CCA TCA CCT  
his tyr val thr leu asn leu pro cys ser leu leu thr pro pro ala ser pro ser pro

782 812  
TCT GTT TCT TCT GCA ACA TCT CAG AGT TCT GGA TTT TCT ACG AAT GTA CAA GAC CAA AAG  
ser val ser ser ala thr ser gln ser ser gly phe ser thr asn val gln asp gln lys

842 872  
ATT GCA AAT ATG TTT GAA TTA TCC GTG CCT TTC CGC CAA CAG CAT TAT TTG GCA GGA CTT  
ile ala asn met phe gln leu ser val pro phe arg gln gln his tyr leu ala gly leu

Cadherin  
|xx EC motif xx|

932  
GTG TTA ACA GAG CTG GCT GTC ATT TTA gac cct gat gct gaa gga ctg TTT GGA TTG CAT  
val leu thr gln leu ala val ile leu asp pro asp ala gln gly leu phe gly leu his

962 992  
AAG AAA GTC ATC AAT ATG GTA CAC AAT TTA CTC TCC AGT CAC GAC TCA GAC CCG CGG TAC  
lys lys val ile asn met val his asn leu leu ser ser his asp ser asp pro arg tyr

1022 1052  
TCT GAC CCT CAG ATA AAG GCT CGA GTG GCC ATG TTG TAT CTA CCT CTG ATT GGT ATT ATC  
ser asp pro gln ile lys ala arg val ala met leu tyr leu pro leu ile gly ile ile

1082 1112  
ATG GAA ACT GTA CCT CAG CTG TAT GAT TTT ACA GAA ACT CAC AAT CAA CGA GGA AGA CCA  
met glu thr val pro gln leu tyr asp phe thr glu thr his asn gln arg gly arg pro

1142 1172  
ATT TGT ATA GCC ACT GAT GAT TAT GAA AGT GAG AGC GGA AGT ATG ATA AGC CAG ACC GTT  
ile cys ile ala thr asp asp tyr gln ser gln ser gly ser met ile ser gln thr val

1202 1232  
GCC ATG GCA ATC GCA GGG ACA TCG GTC CCT CAA CTA ACA AGG CCT GGC AGT TTC CTC CTC  
ala met ala ile ala gly thr ser val pro gln leu thr arg pro gly ser phe leu leu

1262 1292  
ACG TCA ACG AGT GGC AGG CAA CAC ACT ACC TTT TCA GCA GAA TCA AGT CGA AGC CTT TTG  
thr ser thr ser gly arg gln his thr thr phe ser ala glu ser ser arg ser leu leu

1322 1352  
ATC TGT CTA CTT TGG GTT CTC AAA AAT GCA GAT GAA ACA GTT CTA CAG AAG TGG TTT ACA  
ile cys leu leu trp val leu lys asn ala asp glu thr val leu gln lys trp phe thr

1382  
 GAT CTC TCA GTC TTG CAG CTA AAC CGG CTA TTA GAT CTG CTT TAT CTC TGT GTG TCT TGC  
 asp leu ser val leu gln leu asn arg leu leu asp leu leu tyr leu cys val ser cys

1412  
 1442  
 TTT GAG TAT AAA GGG AAA AAA GTG TTT GAA CGA ATG AAT AGC TTG ACC TTT AAG AAA TCA  
 phe gln tyr lys gly lys lys val phe gln arg met asn ser leu thr phe lys lys ser

1472  
 1502  
 AAA GAC ATG AGA GCA AAG CTT GAA GAA GCT ATT CTT GGG AGC ATA GGT GCC AGG CAA GAA  
 lys asp met arg ala lys leu gln gln ala ile leu gly ser ile gly ala arg gln gln

1532  
 1562  
 ATG GTA CGG CGA AGC CGA GGA CAG CTC GAG AGA AGC CCA TCT GGA AGT GCC TTT GGA AGT  
 met val arg arg ser arg gly gln leu gln arg ser pro ser gly ser ala phe gly ser

1592  
 1622  
 CAA GAA AAT TTG AGG TGG AGG AAA GAT ATG ACT CAC TGG CGT CAA AAC ACA GAG AAG CTT  
 gln gln asn leu arg trp arg lys asp met thr his trp arg gln asn thr gln lys leu

1652  
 1682  
 GAC AAA TCA AGA GCA GAG ATT GAA CAC GAA GCA CTG ATT GAT GGA AAC CTG GCT ACA GAA  
 asp lys ser arg ala gln ile gln his gln ala leu ile asp gly asn leu ala thr gln

1712  
 1742  
 GCA AAC CTA ATC ATT TTA GAT ACA TTA GAG ATT GTT GTT CAG ACC GTT TCT GTA ACG GAA  
 ala asn leu ile ile leu asp thr leu gln ile val val gln thr val ser val thr gln

1772  
 1802  
 TCC AAA GAG AGC ATT CTT GGT GGA GTG CTA AAA GTG CTA CTA CAC AGC ATG GCC TGT AAC  
 ser lys gln ser ile leu gly gly val leu lys val leu leu his ser met ala cys asn

1832  
 1862  
 CAA AGT GCA GTT TAT CTA CAA CAC TGT TTT GCT ACA CAG AGA GCC TTG GTT TCA AAG TTT  
 gln ser ala val tyr leu gln his cys phe ala thr gln arg ala leu val ser lys phe

1892  
 1922  
 CCT GAA CTC TTA TTT GAA GAA GAG ACA GAG CAG TGT GCT GAT TTA TGC CTC AGG CTT CTC  
 pro gln leu leu phe gln gln gln thr gln gln cys ala asp leu cys leu arg leu leu

1952  
 1982  
 CGA CAC TGT AGC AGT AGC ATC GGT ACA ATA CGG TCA CAC CCC AGT GCC TCC CTT TAC CTA  
 arg his cys ser ser ser ile gly thr ile arg ser his pro ser ala ser leu tyr leu

2012  
 2042  
 CTA ATG AGG CAA AAC TTT GAG ATT GGG AAT AAC TTT GCC AGG GTT AAA ATG CAG GTA CCA  
 leu met arg gln asn phe gln ile gly asn asn phe ala arg val lys met gln val pro

2072

2102 2132  
ATG TCA CTA TCC TCC TTG GTG GGC ACA TCT CAG AAT TTT AAT GAA GAA TTC TTA AGA CGT  
met ser leu ser ser leu val gly thr ser gln asn phe asn glu glu phe leu arg arg

2162 2192  
TCT CTA AAG ACT ATA TTG ACA TAT GCT GAA GAA GAT CTG GAA TTG AGG GAA ACA ACA TTT  
ser leu lys thr ile leu thr tyr ala glu glu asp leu glu leu arg glu thr thr phe

2222 2252  
CCT GAT CAG GTC CAG GAT CTG GTT TTC AAT CTC CAT ATG ATT CTT TCT GAT ACT GTG AAA  
pro asp gln val gln asp leu val phe asn leu his met ile leu ser asp thr val lys

2282 2312  
ATG AAG GAA CAC CAG GAG GAT CCT GAA ATG TTG ATT GAT CTA ATG tac aga att gcc aag  
met lys glu his gln glu asp pro glu met leu ile asp leu met tyr arg ile ala lys

2342 2372  
ggt tac CAG ACC TCT CCA GAT CTG CGA TTG ACC TGG TTG CAG AAC ATG GCA GGC AAG CAC  
gly tyr gln thr ser pro asp leu arg leu thr trp leu gln asn met ala gly lys his

2402 |XXXXXXXXXXXXXXXXXXXX transmembrane domain XXXXXXXXXXXXXXXXXXXXXXX  
TCA GAA CGA AGC AAT CAT GCT GAA GCT GCA CAG TGT CTA GTC CAC TCA GCA GCA CTT GTT  
ser glu arg ser asn his ala glu ala ala gln cys leu val his ser ala ala leu val  
XXXXXXXXXXXXXXXXXXXX|

2492  
GCT GAA TAT TTG AGC ATG CTG GAG GAC CGG AAA TAT CTT CCT GTG GGA TGT GTA ACA TTT  
ala glu tyr leu ser met leu glu asp arg lys tyr leu pro val gly cys val thr phe

2522 2552  
CAG AAT ATT TCA TCT AAT GTT TTA GAA GAA TCT GCG GTC TCA GAT GAT GTG GTA TCT CCA  
gln asn ile ser ser asn val leu glu glu ser ala val ser asp asp val val ser pro

2582 2612  
GAT GAA GAA GGT ATC TGC TCT GGA AAA TAC TTT ACT GAG TCA GGA CTT GTG GGA TTA CTG  
asp glu glu gly ile cys ser gly lys tyr phe thr glu ser gly leu val gly leu leu

2642 2672 |XXXXX ITAM XXXX| |xxx  
GAA CAA GCA GCT GCT TCC TTC TCT ATG GCT GGC ATG TAT GAA GCA GTT AAT GAA GTT TAC  
glu gln ala ala ala ser phe ser met ala gly met tyr gln ala val asn glu val tyr  
xx ITAM xxx|

2732  
AAA GTA CTT ATT CCT ATT CAT GAA GCT AAT CGG GAT GCA AAG AAA CTA TCC ACA ATT CAT  
lys val leu ile pro ile his glu ala asn arg asp ala lys lys leu ser thr ile his

2762 2792  
GGT AAA CTT CAA GAA GCA TTC AGC AAA ATT GTT CAT CAG AGT ACT GGC TGG GAG CGG ATG  
gly lys leu gln glu ala phe ser lys ile val his gln ser thr gly trp glu arg met

2822 |xxxxx ITAM xxxx| 2852  
TTT GGC ACC TAT TTT CGT GTT GGT TTT TAT GGA ACC AAG TTC GGG GAT TTG GAT GAA CAA  
phe gly thr tyr phe arg val gly phe tyr gly thr lys phe gly asp leu asp glu gln

2882 2912  
GAA TTT GTT TAC AAG GAG CCT GCA ATA ACC AAA CTT GCA GAG ATA TCT CAC AGA TTG GAG  
glu phe val tyr lys glu pro ala ile thr lys leu ala glu ile ser his arg leu glu

2942 2972  
GGA TTT TAC GGA GAA AGA TTT GGA GAG GAT GTG GTT GAA GTA ATC AAA GAC TCT AAT CCT  
gly phe tyr gly glu arg phe gly glu asp val val glu val ile lys asp ser asn pro

3002 3032|xxxxx ITAM xxxx|  
GTA GAC AAG TGT AAA TTA GAT CCT AAC AAG GCA TAT ATT CAG ATT ACC TAT GTG GAG CCA  
val asp lys cys lys leu asp pro asn lys ala tyr ile gln ile thr tyr val glu pro

3062 3092  
TAC TTT GAC ACA TAT GAG ATG AAG GAC AGA ATC ACC TAT TTC GAC AAA AAT TAC AAT CTT  
tyr phe asp thr tyr glu met lys asp arg ile thr tyr phe asp lys asn tyr asn leu

3122 3152  
CGT CGA TTC ATG TAC TGT ACA CCC TTT ACT TTA GAT GGC CGT GCC CAT GGG GAA CTT CAT  
arg arg phe met tyr cys thr pro phe thr leu asp gly arg ala his gly glu leu his

3182 3212  
GAA CAA TTC AAA AGG AAG ACC ATT CTG ACT ACG TCT CAT GCC TTT CCT TAT ATT AAA ACA  
glu gln phe lys arg lys thr ile leu thr thr ser his ala phe pro tyr ile lys thr

3242 3272 |xxxxxxxxxxxxxxxxxxxxxxxxxxxx|  
AGG GTC AAT GTC ACT CAT AAA GAA GAG ATC ATC TTA ACA CCA ATT GAA GTT GCT ATT GAG  
arg val asn val thr his lys glu glu ile ile leu thr pro ile glu val ala ile glu

xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx Coiled coil 1 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx  
GAC ATG CAG AAA AAG ACA CAG GAG TTG GCA TTT GCA ACA CAT CAG GAT CCC GCA GAC CCC  
asp met gln lys lys thr gln glu leu ala phe ala thr his gln asp pro ala asp pro

xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx| 3392  
AAA ATG CTT CAG ATG GTA CTC CAG GGA TCT GTA GGC ACC ACA GTG AAT CAG GGG CCT TTG  
lys met leu gln met val leu gln gly ser val gly thr thr val asn gln gly pro leu

3422 3452  
GAA GTT GCC CAG GTT TTT CTG TCT GAA ATA CCT AGT GAC CCA AAG CTC TTC AGA CAT CAT  
glu val ala gln val phe leu ser glu ile pro ser asp pro lys leu phe arg his his

3482 3512 |xxxxxxxxxxxxx|  
AAT AAA CTG CGA CTC TGC TTT AAA GAT TTT ACT AAA AGG TGT GAA GAT GCC TTA AGA AAA  
asn lys leu arg leu cys phe lys asp phe thr lys arg cys glu asp ala leu arg lys

XXXXXXXXXXXXXXXXXXXXX Coiled coil 2 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX |

AAT AAG AGC TTA ATT GGG CCG GTT CAA AAG GAG TAT CAA AGG GAA TTG GGG AAA CTA TCT  
asn lys ser leu ile gly pro val gln lys glu tyr gln arg glu leu gly lys leu ser

3602

3632

TCG CCT TAA AGA GGC CCT ACA GCC CTA GAT CAC AGA AAG TCC CTC AGT TAT CCA AGC CAG  
ser pro STP

3662

3692

TAT TGC TTG TCC CCT GCC ACA GAG ATT CCT TCA GTC GAA TGA GCT TTC GCA AAA TGG ATC

3722

3752

TCT AAA CTG AAT GCA CTT GTT TTA TTC ATC TGC AAA GAG CCA TGT ATT CAA CAT CGA GTG

3782

3812

TGA AAA GAT CTA TTG GAA ACC AAC ATG GAA TGG AAT TCT GGA AAT TAT TAT TCA TTG AAG

3842

3872

AAT GCA GTG GCC AAG AAA ATA TCA AAT GTA GAT TGT TAA CGC TTG AGA ATC ATG GCT ATG

3902

3932

GTT TCT AAT GTT CGG GTA ACA AGC TGT TAT CTT TTA AGA CAT TTT AAT GAC TCA AAG GTA

3962

3992

CAC TAT ACA TTT ACC ATT ATT TAT ACC ATA GCT AAG GTT AAA AAT TTA TTC ACT TTA AGT

4022

4052

TCG TAT TTT TTA ATT TAT ATC ACC ATT TAT AGA TTC ATT TTG GAC CCA TTT TAA ATG TAG

4082

4112

TAA TGC TTA TTT TAA AGG TAC TAA AAA ATA TGT GAA TGT TTA CCT CGT GCG CGC CAG GGC

4142

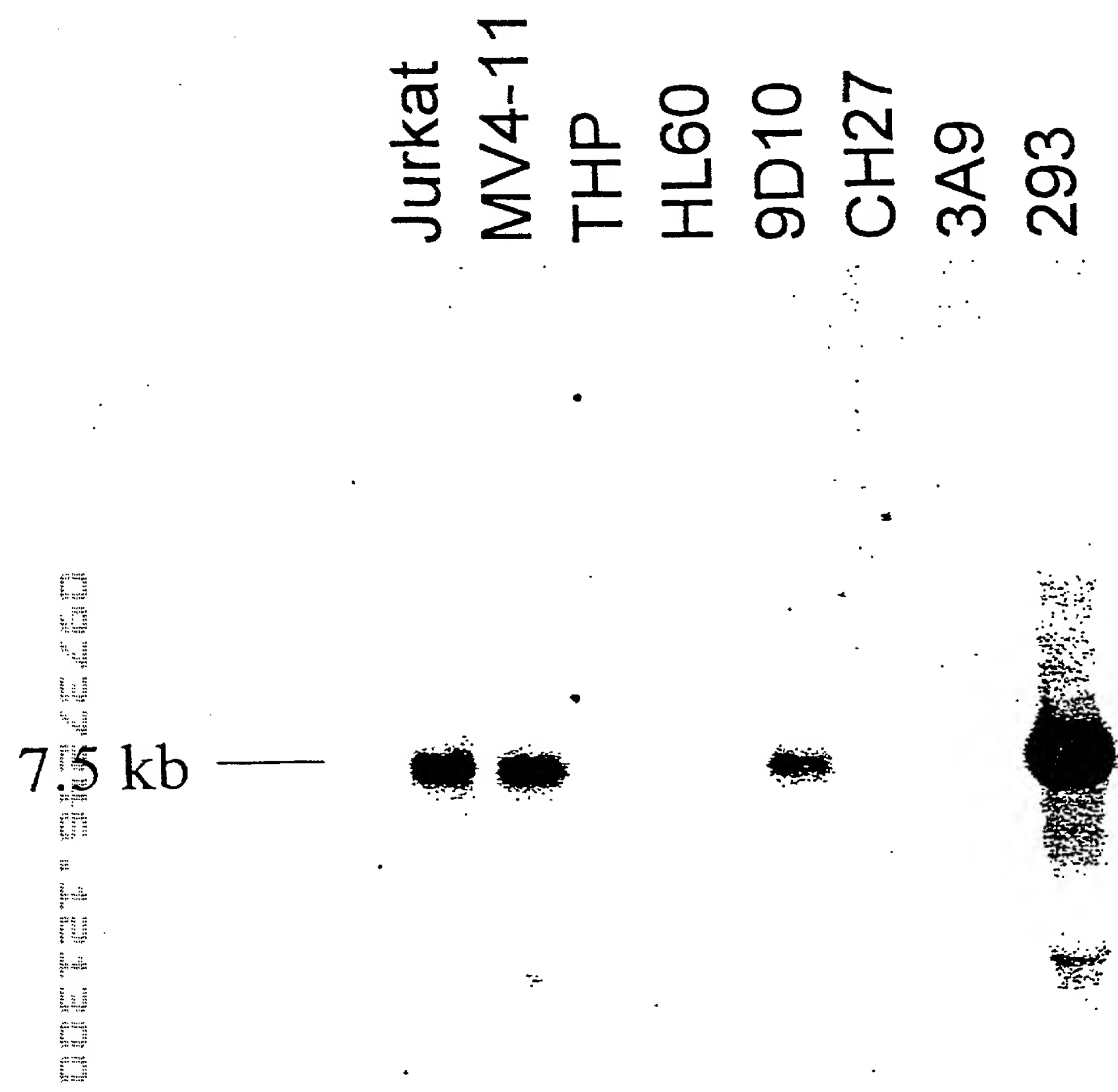
CTC

546 →

PBL  
lung  
placenta  
sm intestine  
liver  
kidney  
spleen  
thymus  
colon  
skel muscle  
heart  
brain



# Human CLASP-3 Multiple Cell Lines Northern





HC2A	-----
KIAA	ASGNLDKNARFS AIYRQDSNKLSNDDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----

HC2A	-----
KIAA	FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLYDSQ
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----

HC2A	-----VLHHHQNP E F Y D E I K
KIAA	KSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVFTRSAFAAVLHHHQNP E F Y D E I K
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----

HC2A	IELPTQLHEKH H L L L T F F H V S C D N S S K G S T K K R D V V E T Q V G Y S W L P L L K D G R V V T S E Q H I
KIAA	IELPTQLHEKH H L L L T F F H V S C D N S S K G S T K K R D V V E T Q V G Y S W L P L L K D G R V V T S E Q H I
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----

HC2A	PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
KIAA	PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
rat	-----
HC4	-----
HC1	-----
HC3	-----GPGPARSTV S I S L I S N S A R V
HC5	-----

HC2A	QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
KIAA	QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
rat	-----
HC4	-----MEIQVLIRFLSVILMQLFWVLPNMIHEDDVPISCPMV
HC1	-----MSFLPIILNQLFKVLV-QNEEDEITTTVTRV
HC3	NRSRSLSNSNPDISGTPTSPDDEVRSIIGSKGLDRSNSWNTGGPKAAPWGSNPSPSAES
HC5	-----

HC2A	I I H V V A Q C H E E G L E S H L R S Y V K Y A Y K A E P Y V A S E Y K T V H E E L T K S M T T I L K P S A D F L T S N
KIAA	I I H V V A Q C H E E G L E S H L R S Y V K Y A Y K A E P Y V A S E Y K T V H E E L T K S M T T I L K P S A D F L T S N
rat	-----
HC4	L F H I V S K C H E E G L D S Y L S S F I K Y S F R P G K P S A P Q A P L I H E T L A T M M I A L L K Q S A D F L A I N
HC1	L P D I V A K C H E E Q L D H S V Q S Y I K F V F K T R --- A C K E R P V H E D L A K N V T G L L K - S N D S P T V K
HC3	T Q A M D R S C N R M S S H T E T S S F L Q T L T G R L P --- T K K L F H E E L A L Q W V V C S G -- S V R --- E
HC5	-----

Cadherin  
Cleavage

HC2A	K L L R Y S W F F F D V L I K S M A Q H L I E N S K V K L I R N Q R F P A S Y H H A A E T V V N M L M P H I T Q K F G D
KIAA	K L L K Y S W F F F D V L I K S M A Q H L I E N S K V K L I R N Q R F P A S Y H H A V E T V V N M L M P H I T Q K F R D
rat	-----
HC4	K L L K Y S W F F F E I I A K S M A T Y L L E E N K I K L T H G Q R F P K A Y H H A L H S L F L A I T - I V E S Q Y A E
HC1	H V L K H S W F F F A I I L K S M A Q H L I D T N K I Q L E R P Q R F P E S Y Q N E L D N L V M V L S D H V I W K Y K D
HC3	S A L Q Q A W F F F E L M V K S M V H H L Y F N D K L E A P R K S R F P E R F M D D I A A L V S T I A S D I V S R F Q K
HC5	-----

HC2A	N P E A S K N A N H S L A V F I K R C F T F M D R G F V F K Q I N --- N Y I S -- C F A P G D P K T L F E Y K F E F L
KIAA	N P E A S K N A N H S L A V F I K R C F T F M D R G F V F K Q I N --- N Y I S -- C F A P G D P K T L F E Y K F E F L
rat	-----
HC4	I P K E S R N V N Y S L A S F L K C C L T L M D R G F V F N L I N --- D Y I S -- G F S P K D P K V L A E Y K F E F L
HC1	A L E E T R R A T H S V A R F L K R C F T F M D R G C V F K M V N --- N Y I S -- M F S S G D L K T L C Q Y K F D F L
HC3	D T E M V E R L N T S L A F F L N D L L S V M D R G F V F S L I K S C Y K Q V S S K L Y S L P N P S V L V S L R L D F L
HC5	-----

HC2A	R V V C N H E H Y I P L N L P M --- P F G K G R I Q R --- Y Q D L Q L --- D Y S L T D E F
KIAA	R V V C N H E H Y I P L N L P M --- P F G K G R I Q R --- Y Q D L Q L --- D Y S L T D E F
rat	-----
HC4	Q T I C N H E H Y I P L N L P M --- A F A K P K L Q R --- V Q D S N L --- E Y S L S D E Y
HC1	Q E V C Q H E H F I P L C L P I R S A N I P D P L T P S E S --- T Q E L H A S D M P E Y S V T N E F
HC3	R I I C S H E H Y V T L N L P C S L L T P P A S P S P S V S S A T S Q S S G F S T N V Q D Q K I A N M F E L S -- V P F
HC5	----- M N A D T A P T S P C P S I S --- S Q N S S S C S S F Q D Q K I A S M F D R T S R V P A

Cadherin  
EC motif

HC2A	C R N H F L V G I L L R E V G T A L Q E F R E --- V R L I A I S V L K N L L I K H S F D D R Y A S R S H Q A R I A T
KIAA	C R N H F L V G I L L R E V G T A L Q E F R E --- V R L I A I S V L K N L L I K H S F D D R Y A S R S H Q A R I A T
rat	-----
HC4	C K H H F L V G I L L R E T S I A L Q D N Y E --- I R Y T A I S V I K N L L I K H A F D T R Y Q H K N Q Q A K I A Q
HC1	C R K H F L I G I L L R E V G F A L Q E D Q D --- V R H L A L A V L K N L M A K H S F D D R Y R E P R K Q A Q I A S
HC3	R Q Q H Y L A G I V L T E L A V I L D P D A E G L F G L H K K V I N M V H N L L S S H D S D P R Y S D P Q I K A R V A M
HC5	S S T S - S P G I L F T E L A A A L D A E G E G I S E V Q R K A V S A I H S L L S S H D L D P R C V K P E V K V K I A A

HC2A	L Y L P L F G L L I E N V Q R I N V R D V S P F P V N A G - M T V K D E S L A L P A V N P L V T P Q K G S T L D N S L H
KIAA	L Y L P L F G L L I E N V Q R I N V R D V S P F P V N A G - M T V K D E S L A L P A V N P L V T P Q K G S T L D N S L H
rat	-----
HC4	L Y L P F V G L L L E N I Q R L A G R D T L Y S C A A M P N S A S R D E F P C G --- F T S P -- A N -- R G S L S
HC1	L Y M P L Y G M L L D N M P R I Y L K D L Y P F T V N T S N Q G S R D D L S T N G G F Q S Q T A I K H A N S V D T S F S
HC3	L Y L P L I G I I M E T V P Q L Y D F T E T H N Q R G R P I C I A T D D Y E S E --- S G --- S M I S
HC5	L Y L P L V G I I L D A L P Q L C D F T V A D T R R Y R --- T S G S D E E Q E --- G A --- G A I T

HC2A	KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDDKHQQSS
KIAA	KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDDKHQQSS
rat	-----
HC4	TDKDTAYGSFQNG-----HGIKREDSRGSLIP-EGATGFPDQGNTGEN-----TRQS
HC1	KDVLNSIAAFSS-----IAISTVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPL
HC3	QTVAMAIAGTSVPQ-----LTRPGSFLLTSTSGRQHT-----
HC5	QNALAIAGNNFN-----LKTSG-IVLSSLPYKQYN-----

HC2A	TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSDDALFTYWN-KASTSELMDFFTISEVCL
KIAA	TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSDDALFTYWN-KASTSELMDFFTISEVCL
rat	-----
HC4	STRSSVSQYNRLDQYEIRSLLMCYLYIVKMISEDTLTYWN-KVSPQELINILILLEVCL
HC1	ALIGSTLRFDRDLQAEIRSLLMCFHIMKTISYETLIAYWQ-RAPSPEVSDFFSILDVCL
HC3	-----TFSAESSRSLICLLWVLKN-ADETVLQKWFTDLSVLQLNRLDLLYLCV
HC5	-----MLNADTTRNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRILDLLFICV

HC2A	HQFQYMCKRYIARNQEGLG--PIVHDRKS-----QTLPVSRNRTGMM
KIAA	HQFQYMCKRYIAR-----TGMM
rat	-----
HC4	FHFRYMGKRNIARVHDAWLSKHFGIDRKS-----QTMPALRNRSGVM
HC1	QNFYRLGKRNIIRKIAAAF--KFVQSTQNNGTGKSNPSCQTSGLLAQWMHSTSRHEGHK
HC3	SCFEYKGGKVFERMNSLTFK--KSKDMRAK-----LEEAILGSIGARQEMV
HC5	LCFEYKGGKQSSDKVSTQVLQ--KSRDVKAR-----LEEALLRGEGERGEMM

HC2A	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
KIAA	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
rat	-----
HC4	QARLQHL-----SSLESS-----FTLNHSSTTTEADIFHQALLEGNTATEVS
HC1	QHRSQTLPIIRGK--NALSNPCL--LQMLDNTMTSNSNEIDIVHHVDTEANIEGEC
HC3	RRSRGQLERSPSGSAFGSQENLRWRKDMTHWRQNTKLDKSRAEIEHEALIDGNLATEAN
HC5	RRRAPGNDRFP-----GLNENLRWKKEQTHWRQANEKLDKTKAELDQREALISGNLATEAH

HC2A	LTALDTLSLFTLAFKNQLLADHGHNPMLKKVFDVYLCFLQKHQSEETALKNVFTALRSLIY
KIAA	LTALDTLSLFTLAFKNQLLADHGHNPMLKKVFDVYLCFLQKHQSEETALKNVFTALRSLIY
rat	-----KLSRGHSPMLKKVFDVYLCFLQKHQSEETALKNVFTALRSLIY
HC4	LTVLDTISFFTQCFKTHFLNNDGHNPLMKKVFDIHLAFLKNGQSEVSLKHVFASLRAFIS
HC1	LTILDVLSLFTQTHQRQLQQCDQNSLMKRGFDTYMLFFQVNSATALKHVFASLRLFVC
HC3	LIILDTLEIVVQTVS--VTES--KESILGGVLKVLHSMACNQSAVYLOHCFATQALVS
HC5	LIILDMQENIIQASS--ALDC--KDSLLGGVLRVLVNSLNCQSTTYLTHCFATLRALIA

HC2A	KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNFDYTGKKSFVRTH
KIAA	KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNFDYTGKKSFVRTH
rat	KFPSTFYEGRADMCASLCYEVLKCCNSKLSSIRTEASQLLYFLMRNFDYTGKKSFVRTH
HC4	KFPSAFFKGRVNMCAAFCEYVLKCCNSKISSTRNEASALLYLLMRNFEYTKRKTFLRTH
HC1	KFPSAFFQGPADLCGSFCYEVLKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSH
HC3	KFPELLFEEETEQCADLCLRLLRHCSSSIGTIRSHPSASLYLLMRQNFIGN--NFARVK
HC5	KFGDLLFEEVEQCQFDLCHQVLHHCSSSMDVTRSQCACATLYLLMRFSFGATS--NFARVK

HC2A	LQVIISVSQLIADVVGIGETRFOQSLSIINNCANSRDLIKHTSFSSDVKDLTKRIRTVLM
KIAA	LQVIISVSQLIADVVGIGETRFOQSLSIINNCANSRDLIKHTSFSSDVKDLTKRIRTVLM
rat	LQVIISLSQLIADVVGIGETRFOQSLSIINNCANSRDLIKHTSFSSDVKDLTKRIRTVLM
HC4	LQIIIAVSQLIADVALSGGSRFQESLFIINNFANSRPMPLARAFPAEVKDLTKRIRTVLM
HC1	LQLIKAVSQLIAD-AGIGGSRFQHS LAITNNFANGDKQMKNSNFPAEVKDLTKRIRTVLM
HC3	MQVPMSLSSLVGTSQNFNEEFLRRSLKTIITYAEEDLELRETTFPDQVQDLVFNLMHLS
HC5	MQVTMSLASLVGRAPDFNEEHLRRSLRTILAYSEEDTAMQMTPTQVEELLCNLNSILY

		Transmembrane
HC2A	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD	SMARIHVKNGLSEAAMCYVHV
KIAA	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD	SMARIHVKNGLSEAAMCYVHV
rat	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD	SMARIHVKNGLSEAAMCYVHV
HC4	ATAQMKEHEKDPEMLIDLQYSLAKSYASTPELRKTWLD	SMAKIHVKNGLFSEAAMCYVHV
HC1	ATAQMKEHEKDPEMLVDLQYSLANSYASTPELRRTWLE	SMAKIHARNGDLSEAAMCYIHI
HC3	DTVKMKEHQEDPEMLIDLMYRIAKGYQTS	PDLRLTLWLQNMAGKHSERSNHAEAAQCLVHS
HC5	DTVKMREFQEDPEMLMDLMYRIAKSYQAS	PDLRLTLWLQNMAEKHTKKKCYTEAAMCLVHA

	domain	SH3	
HC2A	TALVAEYITRKGV-----		FRQGCTAFRVITPN
KIAA	TALVAEYITRKEA-----	VQWEPPLLPHSHSACLRRSRGGVFRQGCTAFRVITPN	
rat	TALVAEYITRKEAD-----	LALQREPPVFPYSHTSCQRKSRGGMFRQGCTAFRVITPN	
HC4	AALVAEFIHRKKL-----		FPNGCSAFKKITPN
HC1	AALIAEYIKRKGWYKVEKIC	TASLLSEDPHPCDSNSLLTTPSGGSMFMSMGWPAFLSITPN	
HC3	AALVAEYISMLED-----		RKYLPGCVTFONISSN
HC5	AALVAEYISMLED-----		HSYLPVGSVSFONISSN

		ITAM
HC2A	IDEEASMMEDVGMQD-----	VHFNEVDLMELLEQCADGLWKAERYELIADIYKLIPIPI
KIAA	IDEEASMMEDVGMQD-----	VHFNEVDLMELLEQCADGLWKAERYELIADIYKLIPIPI
rat	IDEEASMMEDVGMQD-----	VHFNEVDLMELLEQCADGLWKAERLRAGLLTSINSSSP
HC4	IDEEGAMKEDAGMMD-----	VHYSEEVLLLELLEQCVNGLWKAERYETISEISKLIGPI
HC1	IKEEGAAKEDSGMHD-----	TPYNENILVEQLYMCGEFLWKSEYELIADVKNKPIIAV
HC3	VLEESAVSDDVVSPEEGICSGKYFTESGLVGLLEQAAASFSMAGMYEAVNEVYKVLIP	
HC5	VLEESVVSSEDTLSPDEDGVCAGQYFTESGLVGLLEQAAELFSTGGLYETVNEVYKVLIP	

	ITAM	ITAM	ITAM	ITAM
HC2A	YEKRRD-----			
KIAA	YEKRRD	FERLAHL	YDTI	HRAYSKVTEVMHSGRRLLGTYFRVAFFGQAAQYQFTDSETDVE
rat	SMKSGGTLETTHLYDTI	HRFYSKVTEVITR-----	A-----	AGSWDLLPGGLFGQ
HC4	YENRREFENLTQVYRTI	HGAYTKILEVMHTKKRLLG-----		TFFRVAFYGQ
HC1	FEKQDFKLS	LDLYDI	HRSYLKVAE	VNSEKRLFG-----FYRVAFYGQ
HC3	HEANRDAKKLSTIHGKLQEA	FSKIVHQSTGWERMFG-----		TYFRVGFYGFY-
HC5	LEAHREFRKLTLTHSKLQRA	FDSIVNNDH--KRMFG-----		TYFRVGFYGFY-

	ITAM	ITAM
HC2A	-FFEDEDGKEYIYKEPKLTPLSEISQRL	LLKIYSDRFGSENVKMIQDSGKVNPKDLDSKYA
KIAA	GFFEDEDGKEYIYKEPKLTPLSEISQRL	LLKIYSDRFGSENVKMIQDSGKVNPKDLDSKYA
rat	GFFEDEDGKEYIYKEPKLTPLSEISQRL	LLKIYSDRFGSENVKMIQDSGKVNPKDLDSKFA
HC4	SFFEEEDGKEYIYKEPKLTGLSEISLRLVKI	YGERFGTENVKIIQSDKVNKELDPKFA
HC1	GFFEEEDGKEYIYKEPKLTGLSEISQRL	LLKIYADKFGADNVKIIQDSNKNVNPKDLDPKFA
HC3	TKFGDLDEQEFVYKEPAITKLAEISHRLEGFYGER	FGEDVVEVIKDSNPVDKCKLDPNKA
HC5	SKFGDLDEQEFVYKEPAITKLPEISHRLEAFYGO	FGAEFVEVIKDSNPVDKCKLDPNKA

	ITAM
HC2A	YIQVTHVIPFFDEKELQERKTEFERSHNIRREMFEMPFTQTGKRQGGVEEQCKRRTILTA
KIAA	YIQVTHVIPFFDEKELQERKTEFERSHNIRREMFEMPFTQTGKRQGGVEEQCKRRTILTA
rat	YIQVTHVTPFFDEKELQERKTEFERCHNIRREMFEMPFTQTGKRQGGVEEQCKRRTILTA
HC4	HIQVTYVKPYFDDKELTERKTEFERNHNISRFVFEAPYTLGKKQGCIEEQCKRRTILTT
HC1	YIQVTYVTPFFEEKEIEDRKTDFEMHHNINRFVFETPFTLSGKKHGGVAEQCKRRTILTT
HC3	YIQITYVEPYFDYEMKDRITYFDKNYNLRRFMYCTPFTLDGRAHGEHQFKRRTILTT
HC5	YIQITYVEPYFDEYEMKDRITYFEKNFNLRFRMYTTPFTLEGRPRGELHEQYRRNTVLT

Coiled-Coil 1

HC2A	IHC	F	Y	V	K	K	R	I	P	V	M	Y	Q	H	T	D	L	N	E	I	E	V	A	I	D	E	M	S	K	K	V	A	E	L	R	Q	L	C	S	S	A	E	V	D	M	I	K	L	Q	L	K	L	Q	G	S	V			
KIAA	IHC	F	Y	V	K	K	R	I	P	V	M	Y	Q	H	T	D	L	N	E	I	E	V	A	I	D	E	M	S	K	K	V	A	E	L	R	Q	L	C	S	S	A	E	V	D	M	I	K	L	Q	L	K	L	Q	G	S	V			
rat	IHC	F	Y	V	K	K	R	I	P	V	M	Y	Q	H	T	D	L	N	E	I	E	V	A	I	D	E	M	S	K	K	V	A	E	L	H	Q	L	C	S	S	A	E	V	D	M	I	K	L	Q	L	K	L	Q	G	S	V			
HC4	S	N	S	F	Y	V	K	K	R	I	P	I	N	C	E	Q	Q	I	N	L	K	F	I	D	G	A	T	D	E	I	K	D	K	T	A	E	L	Q	K	L	C	S	S	T	D	V	D	M	I	Q	L	Q	L	K	L	Q	G	W	V
HC1	S	H	L	F	Y	V	K	K	R	I	Q	V	I	S	S	S	T	E	L	N	E	I	E	V	A	I	D	E	M	S	R	K	V	S	E	L	N	Q	L	C	T	M	E	E	V	D	M	I	S	L	Q	L	K	L	Q	G	S	V	
HC3	S	H	A	F	P	Y	I	K	T	R	V	N	V	T	H	K	E	E	I	I	L	T	E	I	E	V	A	I	E	D	M	Q	K	T	Q	E	L	A	F	A	T	H	Q	D	P	A	D	P	K	M	L	Q	M	V	L	Q	G	S	V
HC5	M	H	A	F	P	Y	I	K	T	R	I	S	V	I	Q	K	E	E	F	V	L	T	E	I	E	V	A	I	E	D	M	K	K	T	L	Q	L	A	V	A	I	N	Q	E	P	P	D	A	K	M	L	Q	M	V	L	Q	G	S	V

Coiled-Coil 2

HC2A	S	V	Q	V	N	A	G	P	L	A	R	A	F	L	D	D	T	N	T	K	R	Y	P	D	N	K	V	K	L	L	K	E	V	F	R	Q	F	V	E	A	C	G	Q	A	L	A	V	N	E	R	L	I	K	E	D	Q	L	E		
KIAA	S	V	Q	V	N	A	G	P	L	A	R	A	F	L	D	D	T	N	T	K	R	Y	P	D	N	K	V	K	L	L	K	E	V	F	R	Q	F	V	E	A	C	G	Q	A	L	A	V	N	E	R	L	I	K	E	D	Q	L	E		
rat	S	V	Q	V	N	A	G	P	L	A	R	A	F	L	D	D	T	N	T	K	R	Y	P	D	N	K	V	K	L	L	K	E	V	F	R	Q	F	V	E	A	C	G	Q	A	L	A	V	N	E	R	L	I	K	E	D	Q	L	E		
HC4	S	V	Q	V	N	A	G	P	L	A	R	A	F	L	N	D	S	Q	A	S	K	Y	P	P	K	V	S	E	L	K	D	M	F	R	K	F	I	Q	A	C	S	I	A	L	E	L	N	E	R	L	I	K	E	D	Q	V	E			
HC1	S	V	K	V	N	A	G	P	M	A	Y	A	R	A	F	L	E	E	T	N	A	K	K	Y	P	D	N	Q	V	K	L	L	K	E	I	F	R	Q	F	A	D	A	C	G	Q	A	L	D	V	N	E	R	L	I	K	E	D	Q	L	E
HC3	G	T	T	V	N	Q	G	P	L	E	V	A	Q	V	F	L	S	E	I	P	S	D	P	K	L	F	R	H	N	K	L	R	L	C	F	K	D	F	T	K	R	C	E	D	A	L	R	K	N	K	S	L	I	G	P	V	Q	K		
HC5	G	A	T	V	N	Q	G	P	L	E	V	A	Q	V	F	L	A	E	I	P	A	D	P	K	L	Y	R	H	N	K	L	R	L	C	F	K	E	F	I	M	R	C	G	E	A	V	E	K	N	K	R	L	I	T	A	D	Q	R		

Coiled-Coil 2

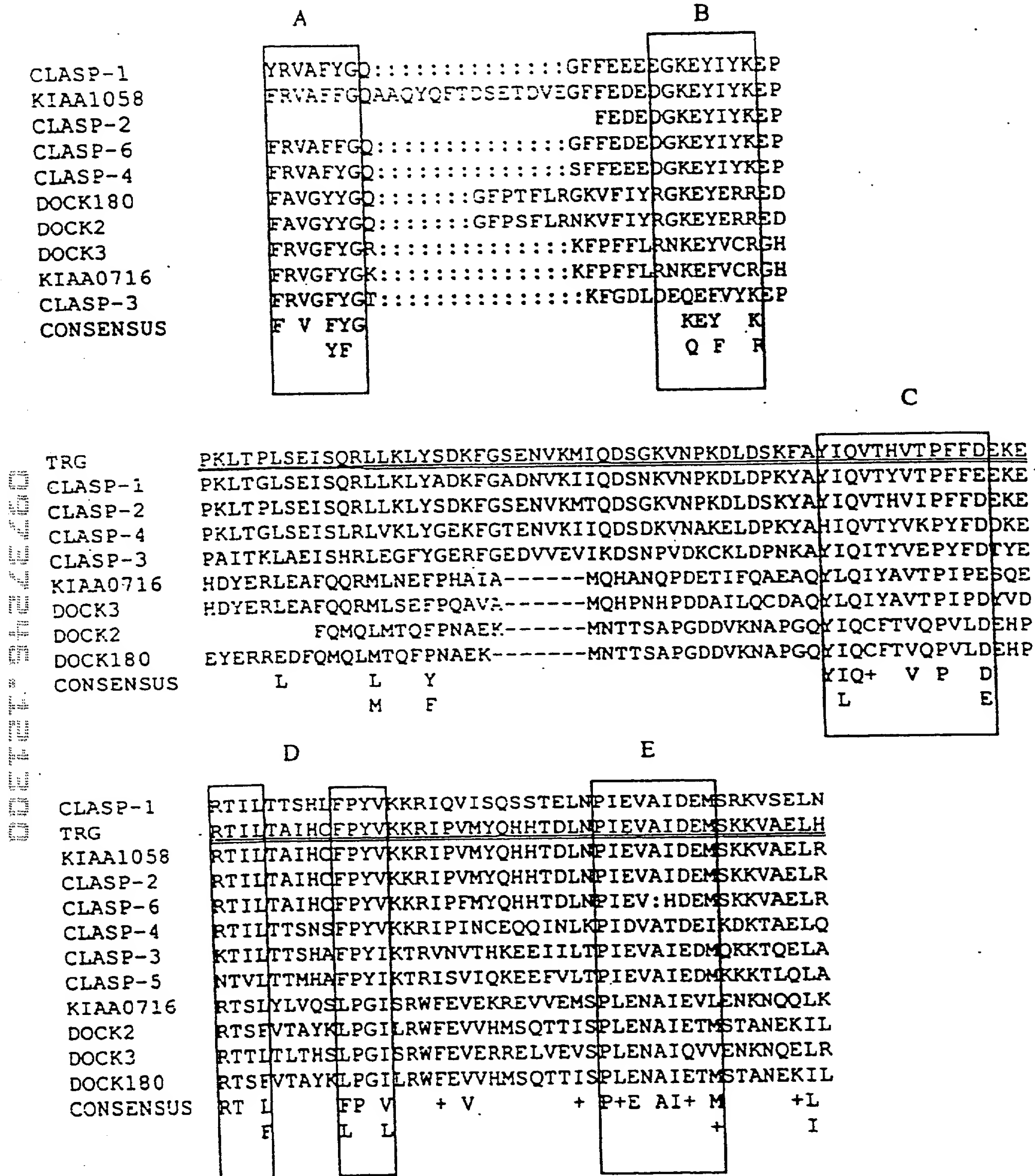
HC2A	Y	Q	E	E	M	K	A	N	Y	R	E	M	A	K	E	L	S	E	I	M	H	E	Q	I	C	P	L	E	E	K	T	S	-	V	L	P	N	S	L	H	I	F	N	A	I	S	G	T	P	T	S	T	M	V	H	G	M	T	S
KIAA	Y	Q	E	E	M	K	A	N	Y	R	E	M	A	K	E	L	S	E	I	M	H	E	Q	L	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-						
rat	Y	Q	E	E	M	K	A	N	Y	R	E	I	R	K	E	L	S	D	I	I	V	E	R	I	C	P	G	E	D	K	R	A	T	K	F	P	A	H	L	Q	R	H	Q	R	D	T	N	K	H	S	G	S	R	V	D	Q	F	I	L
HC4	Y	H	E	G	L	K	S	N	F	R	D	M	V	K	E	L	S	D	I	I	H	E	Q	I	L	Q	E	D	T	M	H	S	P	W	M	S	N	T	L	H	V	F	C	A	I	S	G	T	S	S	D	R	G	Y	G	S	P	R	Y
HC1	Y	Q	E	E	L	R	S	H	Y	K	D	M	L	S	E	L	S	T	V	M	N	E	Q	I	T	G	R	D	D	L	S	K	-	-	-	R	G	V	D	Q	T	C	T	R	V	I	S	K	A	T	P	A	L	P	T	V	S		
HC3	Y	Q	R	E	L	G	-	-	-	-	K	L	S	S	-	-	-	-	-	-	-	-	P	Z	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-								
HC5	Y	Q	Q	E	L	K	K	N	Y	N	K	L	K	E	N	L	R	P	M	I	E	R	K	I	P	E	L	Y	K	P	I	F	R	V	E	S	Q	K	R	D	S	F	H	R	S	S	F	R	K	C	E	T	Q	L	S	Q	G	S	

PBM

HC2A	S	S	V	V	Z	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-								
KIAA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-								
rat	C	V	T	L	P	H	E	P	H	V	G	T	C	F	V	M	C	K	L	R	T	T	F	R	A	N	H	W	F	C	Q	A	Q	E	E	A	M	G	N	G	R	E	K	E	P	W	T	V	I	F	N	S	R	F	Y	R	S	W	G
HC4	E	V	Z	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-								
HC1	S	A	E	V	Z	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-								
HC3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-								
HC5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-								

HC2A	-	-	-	-	-
KIAA	-	-	-	-	-
rat	V	H	I	F	F
HC4	-	-	-	-	-
HC1	-	-	-	-	-
HC3	-	-	-	-	-
HC5	-	-	-	-	-





	F	G
CLASP-1	SLQLKLOGSVSVKVNAG	PMAYARAFLEETNAKKYP
TRG	KLQLKLOGSVSVQVNAG	PLAYARAFLLDDTNTKRY
KIAA1058	KLQLKLOGSVSVQVNAG	PLAYARAFLLDDTNTKRY
CLASP-2	KLQLKLOGSVSVQVNAG	PLAYARAFLLDDTNTKRY
CLASP-6	KLQLKLOGSVSVQVNAG	PLAYARAFLLDDTNTKRY
CLASP-3	MLQMVLOGSVGTTVNQG	PLEVAQVFLSE--IPSDPKLFRHHNK
CLASP-4	QLQLKLOGCVSVQVNAG	PLAYARAFLLNDSQASKYPPKKVSELK
CLASP-5	MLQMVLOGSVGATVNQG	PLEVAQVFLAE--IPADPKLYRHHNK
KIAA0716	PLTMCLNGVIDAAVNGG	VSRYQEAFVKEYILSHPEEDGEKIA
DOCK2	PLSMLLNGIVDPAVMGG	FAKYEKAFFTEEYVRDHPE
DOCK3	LLSMCLNGVIDAAVNGG	IARYQEAFDDKYINKHPGDAEKITQ
DOCK180	PLSMLLNGIVDPAVMGG	FAKYEKAFFTEEYVRDHPEAHEKIEK
CONSENSUS	L M L+G V VN G L I	Y AFL + + P V V F + L+ L I

DOCK1=KIAA0209  
DOCK3=KIAA0299  
CLASP2variant=KIAA1055

2 32  
CGA GTA AAT CGT TCT CGA AGC CTT AGT AAT AGC AAT CCA GAT ATA TCT GGG ACT CCC ACG

62 92  
TCA CCA GAT GAT GAA GTT CGA TCA ATC ATC GGG AGT AAG GGT TTA GAT CGC TCC AAT TCC

122 152  
TGG GTT AAC ACT GGT GGT CCA AAA GCT GCC CCA TGG GGA TCC AAC CCC AGT CCA AGT GCA

182 212  
GAA TCA ACA CAG GCT ATG GAT CGA AGT TGT AAT CGT ATG TCT TCG CAC ACA GAG ACG TCA  
met asp arg ser cys asn arg met ser ser his thr glu thr ser

242 272  
AGT TTC TTA CAA ACA TTA ACG GGA CGC TTA CCA ACT AAA AAG CTT TTT CAC GAG GAG CTG  
ser phe leu gln thr leu thr gly arg leu pro thr lys lys leu phe his glu glu leu

302 332  
GCT TTG CAG TGG GTT GTT TGC AGT GGC AGC GTT CGG GAA TCA GCT TTG CAA CAA GCC TGG  
ala leu gln trp val val cys ser gly ser val arg glu ser ala leu gln gln ala trp  
ref 1.1 and 1.2  
362 ref 2.1 and 2.2 ↓

392  
TTC TTT TTT GAA TTA ATG GTA AAG AGC ATG GTG CAC CAT TTA TAC TTT AAT GAT AAA CTT  
phe phe phe glu leu met val lys ser met val his his leu tyr phe asn asp lys leu

421 452  
GAG GCT CCA AGG AAA AGT CGT TTT CCA GAA CGT TTC ATG GAT GAC ATT GCA GCT CTT GTC  
glu ala pro arg lys ser arg phe pro glu arg phe met asp asp ile ala ala leu val

482 512  
AGC ACG ATT GCT AGT GAT ATA GTT TCA CGA TTT CAG AAG GAC ACA GAA ATG GTT GAG AGA  
ser thr ile ala ser asp ile val ser arg phe gln lys asp thr glu met val glu arg

542 572  
CTC AAT ACA AGC CTT GCA TTC TTT CTC AAT GAT CTG TTG TCT GTT ATG GAC AGA GGA TTT  
leu asn thr ser leu ala phe phe leu asn asp leu leu ser val met asp arg gly phe

602 632  
GTT TTT AGC CTT ATA AAG TCC TGC TAT AAA CAG GTG TCT TCA AAG CTT TAC TCA TTA CCG  
val phe ser leu ile lys ser cys tyr lys gln val ser ser lys leu tyr ser leu pro  
ref 3.1 and 3.2 ↓

662 692  
AAT CCC AGT GTT CTG GTG TCC TTG AGG CTG GAT TTT CTA CGA ATC ATC TGC AGT CAT GAG  
asn pro ser val leu val ser leu arg leu asp phe leu arg ile ile cys ser his glu

722 752  
CAC TAT GTT ACA TTA AAC TTA CCC TGC AGC TTA CTT ACT CCA CCT GCA TCT CCA TCA CCT  
his tyr val thr leu asn leu pro cys ser leu leu thr pro pro ala ser pro ser pro  
ref 4.1 and 4.2 ↓

782 812  
TCT GTT TCT TCT GCA ACA TCT CAG AGT TCT GGA TTT TCT ACG AAT GTA CAA GAC CAA AAG  
ser val ser ser ala thr ser gln ser ser gly phe ser thr asn val gln asp gln lys



842 872  
ATT GCA AAT ATG TTT GAA TTA TCC GTG CCT TTC CGC CAA CAG CAT TAT TTG GCA GGA CTT  
ile ala asn met phe glu leu ser val pro phe arg gln gln his tyr leu ala gly leu

902 932  
GTG TTA ACA GAG CTG GCT GTC ATT TTA gac cct gat gct gaa gga ctg TTT GGA TTG CAT  
val leu thr glu leu ala val ile leu asp pro asp ala glu gly leu phe gly leu his

962 992  
AAG AAA GTC ATC AAT ATG GTA CAC AAT TTA CTC TCC AGT CAC GAC TCA GAC CCG CGG TAC  
lys lys val ile asn met val his asn leu leu ser ser his asp ser asp pro arg tyr

1022 1052  
TCT GAC CCT CAG ATA AAG GCT CGA GTG GCC ATG TTG TAT CTA CCT CTG ATT GGT ATT ATC  
ser asp pro gln ile lys ala arg val ala met leu tyr leu pro leu ile gly ile ile

1082 1112  
ATG GAA ACT GTA CCT CAG CTG TAT GAT TTT ACA GAA ACT CAC AAT CAA CGA GGA AGA CCA  
met glu thr val pro gln leu tyr asp phe thr glu thr his asn gln arg gly arg pro

1142 1172  
ATT TGT ATA GCC ACT GAT GAT TAT GAA AGT GAG AGC GGA AGT ATG ATA AGC CAG ACC GTT  
ile cys ile ala thr asp asp tyr glu ser glu ser gly ser met ile ser gln thr val

1202 1232  
GCC ATG GCA ATC GCA GGG ACA TCG GTC CCT CAA CTA ACA AGG CCT GGC AGT TTC CTC CTC  
ala met ala ile ala gly thr ser val pro gln leu thr arg pro gly ser phe leu leu  
↓ ref5.1 and 5.2

1262 1292  
ACG TCA ACG AGT GGC AGG CAA CAC ACT ACC TTT TCA GCA GAA TCA AGT CGA AGC CTT TTG  
thr ser thr ser gly arg gln his thr thr phe ser ala glu ser ser arg ser leu leu

1322 1352  
ATC TGT CTA CTT TGG GTT CTC AAA AAT GCA GAT GAA ACA GTT CTA CAG AAG TGG TTT ACA  
ile cys leu leu trp val leu lys asn ala asp glu thr val leu gln lys trp phe thr

1382 1412  
GAT CTC TCA GTC TTG CAG CTA AAC CGG CTA TTA GAT CTG CTT TAT CTC TGT GTG TCT TGC  
asp leu ser val leu gln leu asn arg leu leu asp leu leu tyr leu cys val ser cys

1442 1472  
TTT GAG TAT AAA GGG AAA AAA GTG TTT GAA CGA ATG AAT AGC TTG ACC TTT AAG AAA TCA  
phe glu tyr lys gly lys lys val phe glu arg met asn ser leu thr phe lys lys ser

1502 1532  
AAA GAC ATG AGA GCA AAG CTT GAA GAA GCT ATT CTT GGG AGC ATA GGT GCC AGG CAA GAA  
lys asp met arg ala lys leu glu glu ala ile leu gly ser ile gly ala arg gln glu  
↓ ref 6.1 and 6.2

1562 1592  
ATG GTA CGG CGA AGC CGA GGA CAG CTC GAG AGA AGC CCA TCT GGA AGT GCC TTT GGA AGT  
met val arg arg ser arg gly gln leu glu arg ser pro ser gly ser ala phe gly ser

1622 1652  
CAA GAA AAT TTG AGG TGG AGG AAA GAT ATG ACT CAC TGG CGT CAA AAC ACA GAG AAG CTT  
gln glu asn leu arg trp arg lys asp met thr his trp arg gln asn thr glu lys leu

1682	1712
GAC AAA TCA AGA GCA GAG ATT GAA CAC GAA GCA CTG ATT GAT GGA AAC CTG GCT ACA GAA	
asp lys ser arg ala glu ile glu his glu ala leu ile asp gly asn leu ala thr glu	
1742	1772
GCA AAC CTA ATC ATT TTA GAT ACA TTA GAG ATT GTT GTT CAG ACC GTT TCT GTA ACG GAA	
ala asn leu ile ile leu asp thr leu glu ile val val gln thr val ser val thr glu	
1802	1832
TCC AAA GAG AGC ATT CTT GGT GGA GTG CTA AAA GTG CTA CTA CAC AGC ATG GCC TGT AAC	
ser lys glu ser ile leu gly gly val leu lys val leu leu his ser met ala cys asn	
	ref 7.1 and 7.2
1862	1892
CAA AGT GCA GTT TAT CTA CAA CAC TGT TTT GCT ACA CAG AGA GCC TTG GTT TCA AAG TTT	
gln ser ala val tyr leu gln his cys phe ala thr gln arg ala leu val ser lys phe	
1922	1952
CCT GAA CTC TTA TTT GAA GAA GAG ACA GAG CAG TGT GCT GAT TTA TGC CTC AGG CTT CTC	
pro glu leu leu phe glu glu glu thr glu gln cys ala asp leu cys leu arg leu leu	
1982	2012
CGA CAC TGT AGC AGT AGC ATC GGT ACA ATA CGG TCA CAC CCC AGT GCC TCC CTT TAC CTA	
arg his cys ser ser ser ile gly thr ile arg ser his pro ser ala ser leu tyr leu	
2042	2072
CTA ATG AGG CAA AAC TTT GAG ATT GGG AAT AAC TTT GCC AGG GTT AAA ATG CAG GTA CCA	
leu met arg gln asn phe glu ile gly asn asn phe ala arg val lys met gln val pro	
2102	2132
ATG TCA CTA TCC TCC TTG GTG GGC ACA TCT CAG AAT TTT AAT GAA GAA TTC TTA AGA CGT	
met ser leu ser ser leu val gly thr ser gln asn phe asn glu glu phe leu arg arg	
2162	2192
TCT CTA AAG ACT ATA TTG ACA TAT GCT GAA GAA GAT CTG GAA TTG AGG GAA ACA ACA TTT	
ser leu lys thr ile leu thr tyr ala glu glu asp leu glu leu arg glu thr thr phe	
2222	2252
CCT GAT CAG GTC CAG GAT CTG GTT TTC AAT CTC CAT ATG ATT CTT TCT GAT ACT GTG AAA	
pro asp gln val gln asp leu val phe asn leu his met ile leu ser asp thr val lys	
2282	2312
ATG AAG GAA CAC CAG GAG GAT CCT GAA ATG TTG ATT GAT CTA ATG tac aga att gcc aag	
met lys glu his gln glu asp pro glu met leu ile asp leu met tyr arg ile ala lys	
2342	2372
ggt tac CAG ACC TCT CCA GAT CTG CGA TTG ACC TGG TTG CAG AAC ATG GCA GGC AAG CAC	
gly tyr gln thr ser pro asp leu arg leu thr trp leu gln asn met ala gly lys his	
2402	2432
TCA GAA CGA AGC AAT CAT GCT GAA GCT GCA CAG TGT CTA GTC CAC TCA GCA GCA CTT GTT	
ser glu arg ser asn his ala glu ala ala gln cys leu val his ser ala ala leu val	
2462	2492
GCT GAA TAT TTG AGC ATG CTG GAG GAC CGG AAA TAT CTT CCT GTG GGA TGT GTA ACA TTT	
ala glu tyr leu ser met leu glu asp arg lys tyr leu pro val gly cys val thr phe	

↓ ref 8.1 and 8.2

2552  
CAG AAT ATT TCA TCT AAT GTT TTA GAA GAA TCT GCG GTC TCA GAT GAT GTG GTA TCT CCA  
gln asn ile ser ser asn val leu glu glu ser ala val ser asp asp val val ser pro

2582 2612  
GAT GAA GAA GGT ATC TGC TCT GGA AAA TAC TTT ACT GAG TCA GGA CTT GTG GGA TTA CTG  
asp glu glu gly ile cys ser gly lys tyr phe thr glu ser gly leu val gly leu leu

2642 2672  
GAA CAA GCA GCT GCT TCC TTC TCT ATG GCT GGC ATG TAT GAA GCA GTT AAT GAA GTT TAC  
glu gln ala ala ala ser phe ser met ala gly met tyr glu ala val asn glu val tyr

2702 2732  
AAA GTA CTT ATT CCT ATT CAT GAA GCT AAT CGG GAT GCA AAG AAA CTA TCC ACA ATT CAT  
lys val leu ile pro ile his glu ala asn arg asp ala lys lys leu ser thr ile his  
↓ ref 9.1

2762 2792  
GGT AAA CTT CAA GAA GCA TTC AGC AAA ATT GTT CAT CAG AGT ACT GGC TGG GAG CGG ATG  
gly lys leu gln glu ala phe ser lys ile val his gln ser thr gly trp glu arg met

2822 2852  
TTT GGC ACC TAT TTT CGT GTT GGT TTT TAT GGA ACC AAG TTC GGG GAT TTG GAT GAA CAA  
phe gly thr tyr phe arg val gly phe tyr gly thr lys phe gly asp leu asp glu gln

2882 2912  
GAA TTT GTT TAC AAG GAG CCT GCA ATA ACC AAA CTT GCA GAG ATA TCT CAC AGA TTG GAG  
glu phe val tyr lys glu pro ala ile thr lys leu ala glu ile ser his arg leu glu  
↓ ref 10.1 and 10.2

2945 2972  
GGA TTT TAC GGA GAA AGA TTT GGA GAG GAT GTG GTT GAA GTA ATC AAA GAC TCT AAT CCT  
gly phe tyr gly glu arg phe gly glu asp val val glu val ile lys asp ser asn pro

3002 3032  
GTA GAC AAG TGT AAA TTA GAT CCT AAC AAG GCA TAT ATT CAG ATT ACC TAT GTG GAG CCA  
val asp lys cys lys leu asp pro asn lys ala tyr ile gln ile thr tyr val glu pro

3062 3092  
TAC TTT GAC ACA TAT GAG ATG AAG GAC AGA ATC ACC TAT TTC GAC AAA AAT TAC AAT CTT  
tyr phe asp thr tyr glu met lys asp arg ile thr tyr phe asp lys asn tyr asn leu

3122 3152  
CGT CGA TTC ATG TAC TGT ACA CCC TTT ACT TTA GAT GGC CGT GCC CAT GGG GAA CTT CAT  
arg arg phe met tyr cys thr pro phe thr leu asp gly arg ala his gly glu leu his

3182 3212  
GAA CAA TTC AAA AGG AAG ACC ATT CTG ACT ACG TCT CAT GCC TTT CCT TAT ATT AAA ACA  
glu gln phe lys arg lys thr ile leu thr thr ser his ala phe pro tyr ile lys thr  
↓ ref 11.1

3242 3272  
AGG GTC AAT GTC ACT CAT AAA GAA GAG ATC ATC TTA ACA CCA ATT GAA GTT GCT ATT GAG  
arg val asn val thr his lys glu glu ile ile leu thr pro ile glu val ala ile glu

3302	3332
GAC ATG CAG AAA AAG ACA CAG GAG TTG GCA TTT GCA ACA CAT CAG GAT CCC GCA GAC CCC	
asp met gln lys lys thr gln glu leu ala phe ala thr his gln asp pro ala asp pro	
3362	3392
AAA ATG CTT CAG ATG GTA CTC CAG GGA TCT GTA GGC ACC ACA GTG AAT CAG GGG CCT TTG	
lys met leu gln met val leu gln gly ser val gly thr thr val asn gln gly pro leu	
3422	3452
GAA GTT GCC CAG GTT TTT CTG TCT GAA ATA CCT AGT GAC CCA AAG CTC TTC AGA CAT CAT	
glu val ala gln val phe leu ser glu ile pro ser asp pro lys leu phe arg his his	
3482	3512
AAT AAA CTG CGA CTC TGC TTT AAA GAT TTT ACT AAA AGG TGT GAA GAT GCC TTA AGA AAA	
asn lys leu arg leu cys phe lys asp phe thr lys arg cys glu asp ala leu arg lys	
3542	3572
AAT AAG AGC TTA ATT GGG CCG GTT CAA AAG GAG TAT CAA AGG GAA TTG GGG AAA CTA TCT	
asn lys ser leu ile gly pro val gln lys glu tyr gln arg glu leu gly lys leu ser	
3602	3632
TCG CCT TAA AGA GGC CCT ACA GCC CTA GAT CAC AGA AAG TCC CTC AGT TAT CCA AGC CAG	
ser pro OCH	
3662	3692
TAT TGC TTG TCC CCT GCC ACA GAG ATT CCT TCA GTC GAA TGA GCT TTC GCA AAA TGG ATC	
3722	3752
TCT AAA CTG AAT GCA CTT GTT TTA TTC ATC TGC AAA GAG CCA TGT ATT CAA CAT CGA GTG	
3782	3812
TGA AAA GAT CTA TTG GAA ACC AAC ATG GAA TGG AAT TCT GGA AAT TAT TAT TCA TTG AAG	
3842	3872
AAT GCA GTG GCC AAG AAA ATA TCA AAT GTA GAT TGT TAA CGC TTG AGA ATC ATG GCT ATG	
3902	3932
GTT TCT AAT GTT CGG GTA ACA AGC TGT TAT CTT TTA AGA CAT TTT AAT GAC TCA AAG GTA	
3962	3992
CAC TAT ACA TTT ACC ATT ATT TAT ACC ATA GCT AAG GTT AAA AAT TTA TTC ACT TTA AGT	
4022	4052
TCG TAT TTT TTA ATT TAT ATC ACC ATT TAT AGA TTC ATT TTG GAC CCA TTT TAA ATG TAG	
	ref 12.1
4082	4112
TAA TGC TTA TTT TAA AGG TAC TAA AAA ATA TGT GAA TGT TTA CCT CGT GCG CGC CAG GGC	
4142	
CTC	

### Ref 1.1

Sequence of BAC8 using primer C3S3, which spans nucleotides 340-359 of the cDNA. Exon sequence is underlined and represents nucleotides 364-380.

TTTTTGAATTAATGGTGAGCAAAAACTGAGCATGTTCTTTAATATTTTTTCTCTTAGTG  
AACAAATTTTATGCTAGCTCATTTGTTACCTTAGAAATCTTTTTCTGTTGCACATCTTAAC  
GCTTTTCCATGTGCCTCTAAGACAAAATTACATGTGTTACATCTCTAAATAAACACTGT  
GGACACTCAACACAGTTTAGGTGGAATTAAGAGTGAGGCTCATTTTAACTCTTATTTTC  
TCAGGGATGGTTGCATAAGCTAGCTATATTTTCAAAGGAAACTTGTGATACATTCTTTG  
CTAGTCATTATACATGAAGTGTATAATGACAGTATTGTAGATTTTATACCAAAGATGG  
AAAGAGCTTTATAGATACCCACTGCTATTGTTATGGCTAGTAAACCCTTAGGGAAATG  
CCAGTTACAATCAATAAAAAACAACAGTCTGGCTGGGTGCAGTGGCTCACACCTGTA  
ATCTCAGCACTTTAGAAGGCCGAGGCAGGAGGATCACTTGAGATCAGGAGTTTGAGAC  
CCAGCCTGGGCAACATAGCAAGAGCCCATATNTACCCAAAAAAAATTTTTTTTTTAAAT  
TAAGCTAAAACCCTGGNNGGCCACAAAACCTGTAGTTCCCATCTACTTTGGAAAGGCT  
TGAAGGANGGGAGGGCTTGCTTTGAGCCCCAAGAANGTTCAAAGGCTNGCNGNCAGG  
TTNTGATTCNACACNTGCAACTCCCGCATTGGGTNAACAAAANCCAAGGAANC.

### Ref 1.2

Sequence of BAC9 using primer C3S3, which spans nucleotides 340-359 of the cDNA. Exon sequence is underlined and represents nucleotides 371-380.

AATTAATGGTGAGCAAAAACTGAGCATGTTCTTTAATATTTTTTCTCTTAGTGAACAAT  
TTTATGCTAGCTCATTTGTTACCTTAGAAATCTTTTTCTGTTGCACATCTTAACGCTTTT  
CCATGTGCCTCTAAGACAAAATTACATGTGTTACATCTCTAAATAAACACTGTGGACA  
CTCAACACAGTTTAGGTGGAATTAAGAGTGAGGCTCATTTTAACTCTTATTTTCTCAGG  
GATGGTTGCATAAGCTAGCTATATTTTCAAAGGAAACTTGTGATACATTCTTTGCTAGT  
CATTATACATGAAGTGTATAATGACAGTATTGTAGATTTTATACCAAAGATGGAAAGA  
GCTTTATAGATACCCACTGCTATTGTTNTGGCTAGTAAACCCTTANGGAAATGCCAGTT  
NCAATCAATAAAAAACAACAGTACTGGCTGGGTGCAGTGGCTTACACCTGTAATCTC  
AGCACTTTATAAGGCCCNAGGCNNGGAGGATCACTTNAGATCCAGGAGTTTGAGACCAG  
CCTGGGCAACATANCAAGAGCCCATTATCTACCAAAAAAANTTTTTTTTTTAAAATTAAG  
CTAAACNCTGGGTGGNACAAACCTGTTNGNTTCCNATNTNCCTTTGGAAAAGCTTANG  
AAGGGGAGGGCTTNCTTTGGANCCCCAAAAAGTTNAAAGGGNTTGCAGTCAGCCTTTT  
NAATCACCCNNNGGNCCTNTCGCATTGGGATTNCCAANANGCCAANGNAACCCCGNT  
CNTNTTTTAAAAAANTNTTTTAAAGNANNTTTNTTNGN



### Ref 2.1

Sequence of BAC8 using primer HC3AS7, which spans nucleotides 386-405 of the cDNA. Exon sequence is underlined and represents nucleotides 381-385.

TCTTTNGAAAAAGATTANATTATTAATTCTATGATATATTAACAATACACANCTCTAA  
CACTTGGACTATTTTTTAAAATATGGCATGTAATTTAATAGATGACTGAAATATTTTAGC  
TTCTCAAATATTTTTTAAAGTTCCCTACAATGTTTTGTATTTGCTTAAAATAAAATANA  
AAAACCACCATATTACTTTTCAGAAAATTATGCTAGCTAACAATAGGACAAAAAATTCT  
GTGTATGTCAACAAAAAAATTCAACCTTAAATTTTTTTTTTCCATAAAAAACAGGGC  
TACTTGCCCAGGTGAGANGTGCTGCCGTATGAGCTCCTCGNTAGATTGCGCNGCCGGA  
NTGTCGGNCCCTNCGTTTAAATATAACGGCGTGNGCNTGTACCGCAGGCTNTGCTAGGT  
CGTGNTCCCAAGATATCNTNTNTANCATANTAGACGNTGGNGNCGNNTGCATGTGGCN  
TNATTNTNGCAATTGTNACAATCCTAGTNTGTACNTNANAGNTCNGCCNCTGTGANNT  
CGTTGTATAGTCNGNGGCNCGCTTGNTTCTGATGCTGAGAGCANTNNCENNACTNTTNN  
NCNCCCATCTTTNCNNTTNNNNNCCCCCNNTTNNATNNTTTNNNTNNCNNNNNNNATNT  
NTNAANNNACCNC

### Ref 2.2

Sequence of BAC9 using primer HC3AS7, which spans nucleotides 386-405 of the cDNA. Exon sequence is not found within this sequence. Since the primer is directed against exon sequence we presume that sequence derived from HC3AS7 is intron sequence. Additionally, this sequence matches the intron sequence found in the previous sequence (BAC8 sequenced with HC3AS7).

GCGCTNCCNNNTNNTTTATCTTCTGAAAAGACTNATATNATTCTATGATTATAACATTA  
CACACTCTAACACTGGACTTNTTAAATATGGATGTAATTAATAGATGACTGAATATTTT  
AGCTTCTCAAATATNTTTAANGTCCCTACAATGTTTGNATNTGCTTAAAATAAAATANA  
AAACCCCATATTACTTTTCAGAAAANTATGCTAGCTAACAATAGGACANAAAAAATTCTG  
TGTATGCAACAAAAAAATTCAACCTTNAATCTTCTTTTTTTTCCAATANAAAACAGG  
GCTACTCTGCCACAGGCTGGAGTCAGTGGCTGATACAGCTACTGCAGCTCACTCCGGG  
CTATGTGATTGCCTGCCTAAGCCTCNGAGTAGTAGGCTCAGGTGCCACTACATGCCAG  
TAATCTAAAATTTATAGAGACAGGGCTGCTGTGTGNCCAGGCTGGCTAACTCCGGGGCT  
AAGCGTTCTTGCCTNGCTCTAAATGTGGGATACAGNATGTATCATNCATCAGCCAAAA  
AGTTAATTAANTTCCAGATNANTATTTGCATCAAAGCTCCAATNTAGCTTGAAGTAGA  
ACCTGCTCNTTGGCTAGANTATCCCGNNTGTTATGGATCATATTANGCNNTTGTGATGC  
CGAATGGNATCTATTCCGGGAGACANATTACTATNGGATGANAGCANATNGCCCNAT  
GCTTNTTTGTAACGCTNNANNTAAGAACNTTCTNGACATCGTCATAGNTCGAAGTNNT  
NNGCGANTTGATACTAANTTCATGNTANGCCNATGACTNTNGTGATTNNTGANTGNCT  
GGGAGAACCTACNTNCCCCNTACNNATANNCTNCACCCCTACTACTNTNNCNCNTCNC  
TCTCTANTTCTACTCCACNTTATTATCCTCNNCCTTCNCATCNTCCCATCNTNATTCNAC  
GCCNCNANACTTANCNTTNTATNCACTCTNNCT

### Ref 3.1

Sequence of BAC8 using primer C3AS4, which spans nucleotides 737-756 of the cDNA. Exon sequence is underlined and represents nucleotides 677-733.

TAATGTACATAGTGCTCATGACTGCAGATGATTCGTAGAAAATCCAGCCTCAAGGACA  
CCAGAACACTGGGATTCGGTAATGAGTAAAGCTTTGAAGACACCTTGTAAGCAATGCA  
TAAGTAAGAGAACACCAATTGAATCTATTATTTCTTTAATACTAATACCAGAATGGCA  
AATTAGAATTAAAGAGATAGTACTTGGTATCCAGTTTGGGTTTTGTGGCTTAAGTAGCA  
GTATCACCTTTTTCCAGAGTTACTGCTAAAATTAAAAATTTTAAACTATCAGGTTTACT  
GTATAACATATTTGACTAACCTAAAAGCCACATTCTTGTATTTCCAATATAGCATCAA  
TATTTCTACTTCTCATAAAACAGGGGAAAACGTATATCACCAAAAATAACTTCTTATTAC  
TTCCTTCTTAAAAGAAATTATCAATTCTTTTTATAGCACTTTGTGCTTACCTGTATTTAT  
AATTTGTCTGTTTTCTCAGCAACATCATAAGCTACTTGAGGAGACATACTATAAACTGA  
TTTAACAGCTTTAGTGTCCCTACAGCTTAGCTCAATGTTTGACAAATATAGGAGATCAA  
TGCTTAAAGGAATAAAGGCCAGGACAAGTTCTGGTAGCAAATAGTCCATAAAAAGGTTT  
TGGGGGAAAAGGGTAAAAATGGATACATATCGGGGTNGCAAGNTTTTTCCATGTGGG  
GTGAGGTGCCCCATGCCTT

### Ref 3.2

Sequence of BAC9 using primer C3AS4, which spans nucleotides 737-756 of the cDNA. Exon sequence is underlined and represents nucleotides 677-730.

TAACATAGTGCTCTGACTGCAGATGATTCGTAGAAAATCCAGCCTCAAGGACACCAGA  
ACACTGGGATTCGGTAATGAGTAAAGCTTTGAAGACACCTTGTAAGCAATGCATAAGT  
AAGAGAACACCAATTGAATCTATTATTTCTTTAATACTAATACCAGAATGGCAAATTA  
GAATTAAAGAGATAGTACTTGGTATCCAGTTTGGGTTTTGTGGCTTAAGTAGCAGTATC  
ACCTTTTTCCAGAGTTACTGCTAAAATTAAAAATTTTAAACTATCAGGTTTACTGTATA  
AACATATTTGACTAACCTAAAAGCCACATTCTTGTATTTCCAATATAGCATCAATATTT  
CTACTTCTCATAAAACAGGGGAAAACGTATNTCACCAAAAATAACTTCTTATTACTTCCT  
TCTTAAAAAGAAATTATCAATTCTTTTTATAGCACTTTGTGCTTACCCTGNATTTATAAT  
TTGNCTGNTTTTCTCAGCAAACATCATAAGCTACTTGAGGGAGACATACTATTAAACCT  
GATTACAGCTTTTANGTGTCCCTACAGCTTAACTCAATGTTTTGCAAAATNTNNGGAGA  
TCAATGGCTTTAAAGAATAAAAGANCAGGGACAAGTTNTGGGTNGCCATNAGNACAA  
TAAAGGTTTTNNGGGGAAAAGGGGAAAAAATNGATTNCATNTCGNNGGTNGCAAGGTN  
TTTTCCATTGNGGGGNGGAGGGGGCCCATGCCATAANTTTTAACTTTCTTTTTTNGAAG  
AAATTAAACNNTTAAAGGGGTN

### Ref 4.1

Sequence of BAC8 using primer HC3AS6, which spans nucleotides 924-944 of the cDNA. Exon sequence is underlined and represents nucleotides 802-917.

CCAGTCTGCAATATGCTGTGCGAAGCCGATATCAACTTTGCATCTTTGTCTTGNCATTC  
GAGAAATCAGACTTGTGGAAGTAGGAGACAGCTTACAGCGTGCACAAGCTCTCAGCA  
GAGCATATACGAATGAATCTTTTCCAGGGAGTTATTTATATACTACCTGAGCAAGCCA  
CTTAGCTTTGGGCAGGAACCTTNTGGATGTTATAAGTAATACTTATATGAATAATATGA  
AATTAATATTTACTTCTTTTACANTCTTCTCTTTTCTTATCTTAGCCTTTATCCCCTTGT  
GGAAAAGACACTATCAATGCTAGATNCTCCCAAGNCAGAGAATTATGCAGGTTTGGTC  
AGAGAATCGACACAGACATGTTTACAGATTCTTCTTGAAATACATATTGTGCACGAGT  
TTTTTACANTATCTCAATTTAGATCTCAGACAGCATNTNGACTAGNGGGTCTAGGACAT  
AGATACATNTTTGNGAACTTCTATAGAANAACNTNTGCNTTAAAAAGGAGCTTGTTNG  
ANANGAATNNNCTGNGAAGGGCCCGATACGANAAATTTGACTTCGGNGAAAATTNNNG  
GATTNNTACAAANTTCTAGGNGGCACCTTNAANAANGNNTGGGNACNTTGGNGGCGGA  
AAAAAAGCCCTTCNTTTAGNTNTCCCNGAAATGGAAAAGTNCCAANTTCCNAAAAAA  
ANGGGCTTTGTTNNCTTNCNANA

#### Ref 4.2

Sequence of BAC9 using primer HC3AS6, which spans nucleotides 924-944 of the cDNA. Exon sequence is underlined and represents nucleotides 802-921.

GACGCCAGCTCTGTACACAGTCTGCAATATGCTGTGCGGAAGGCCGATATCAACTATT  
GCATCTTTGTCTNGNCATCGAGAAATCAGACTCTGTGGAAGNAGGCAGACAAGACTAT  
ACAGCNTGCACANAGCATCTCAGCAGGCATATAAGAATGAANCTTTTCCAGGGAGTTA  
TTTATATACTACCTGAGCAAGNACTTCAACTTNGGCAGGAACCTTGTGGATGNTTATAA  
GTATACTTATATGAATAANATNGAAATTAATATTTAATTCTTTTACTTCTTCTTTTCC  
TTATCTTAGCCTTTATCCCCTCGTGAAAAAGAGCACTAATCAATGCTATTNCTNCCAAG  
NCAGGAATTTATAGCAGGTTGGTCGAGAATCGACACGACATGTTTACAGANTCATCTT  
GAATACATNATTGTGCACGAGTNTTTTACTCTATCTCAAAATATAGATCTCAGATCGTC  
TATNGANTATGNGGTTCTAGGACATGATTACATTTTNGGGAACTTCCATAGAATAAA  
CNTNTACCTNAAAAANANGAGCCTGTTNGAAATNGAATCTACTNCTAAAGGGCNAGTNC  
CANATTTTACTTCCGCGANATNTCNGGATGTTACAAGTCTAGGGGGNCTTTAGNACGT  
TNGATNTTTGANCGGAAAAAAGCCCTTCTANNGGTCNCCTAATGGAAGCGCCAATTCC  
NAANAAGGNCTGTGTTNTTNGACATTTACCNGNNCCNTTTCTAATCAAACNTNCTCTTC  
TNNANCCNCANCNCNNCCTATANNCTATCNCTCNNCTNNNCTCNTCACTCTCNC  
NCTNTCTTCCNTTCTNCACTNTNNNNTCNCTNNNATNNNCTTCTCCNATCCNTCTCANN  
NNNTCANNCTCCCTACNNTNCNCNTNTTACCATCTNCNCCNNCCT

#### Ref 5.1

Sequence of BAC8 using primer C3S6, which spans nucleotides 1127-1146 of the cDNA. Exon sequence is underlined and represents nucleotides 1181-1269.

GTATGATCCGCCAGACCGCTGCCATGGCAATNGTAGGGACATCGGTCCCTCAACTAAC  
AAGGCCTGGCAGTTTCTNCTCACGTCAACGGTCAAAACAATCCTTCTACAGAATTTT



TTTTCTNGAAAGACAAATATTTACTAGGATATGCCCTTAAATATATGAGATGATTGTAT  
CAGCTGATGCAAAAGTGCTCAGTTTTATTTATGAAAATATTAAAGTTCCCAGAATATTA  
ACTGTCTTCTCCCAAACAGTTTTAAAAAATGATTACCTCAAGGTTTATGGGAAAAAGC  
CCCGTATTCTGCATTTCAGAAATTTGGAAAATTGCCTCATTATAGATAGCCATNTCTTTTTT  
TTNTTTTTTTTTATNCTTCAAGTCTTAGGGNACATGTGCACAACATGCAGGNTAGTTACA  
TATGTATACATGTGCCATGTTGGTGTGCTGCACCCANNAACCCGCAATTTAACATTAGG  
TNTATCTCCAAATGCTATCCNTTCACCCTTCCCCCATNCCACAACAAGGCCCCGGGCNT  
TGNGATGTTCCCCTTCCTGTGCCCACTGTGTNTCACATTNCCNCTTCCCNCCCTTANTN  
NNGTGCAGAACNTNGCCNGTNGCCCTNTNTTTTTTNCCCC

### Ref 5.2

Sequence of BAC9 using primer C3S6, which spans nucleotides 1127-1146 of the cDNA. Exon sequence is underlined and represents nucleotides 1151-1269.

CCNCTGATGATTATGAAAGTGAGAGCGGAAGTATGATAAGCCAGACCGTTGCCATGGC  
AATCGCAGGGACATCGGTCCCTCAACTAACAAGGCCTGGCAGTTTCCTCCTCACGTCA  
ACGGTAAAAACAATCCTCCTACAGAATTTTTTTTTCTAGAAAGACAAATATTTACTAGG  
ATATGCCCTTAAATATATGAGATGATTGTATCAGCTTGATGCAAAAAGTGCTCAGGTTT  
ATTTATGAAAATATTAAAGTTCCAGAATATTTAACTGTCTTCTCCCAAACAGTTTTAAAA  
AATGATACCTCAGGTTTATGGGGAAAAAAGCCCCGTATTCTGTCAATTCAGAAATTTGG  
AAAATTTGNCTCATTATAGATAGTTCATTTTCTTTTTTTTTTTTTTTTTTATACNTTTAA  
AGTTTTTAAGGGGNACCATGTTGCACCAAANATTGCAGGGGTTNGGTTACCATTATGG  
TTATTNCCATTGGTNCCCCCANTGTTTGGGGNGTTGGCTTTGCCACCCCCCAGNGTAAA  
ACCNCCGNTGCGAATTTTTTAAAACAANTTTTGGGGGTTATTANTTNTTTCCCAAAAAT  
NGGCNTTTTTNCCCTTTNCCCCCCTTTCNCCCNCCCNNTTCCCAACNNANCAAGGGGCC  
CCCCGGGTANTGGGGGAATAGNTTCCCCCCCCTTNCCCTNGNNGGGCCAATTGTGGGG  
NNNCTCCATTTGGNNTGCAAANTTCCCCCACCCNTNATTGTTGGTGGNGAAACCATTTT  
CCGGGGGGTTTGGGGGTTTTTTTTTGGTCCCCNTTGCCCAANTAATTTTTGCNTTGAANA  
AAAAGAATGGGGTTTTCCAAAGCTTTTNGTCNCCATTGNTCCCTTTANGGNCCNTTN  
GTTNCCTTNCCANAANGGGCCAATGTGAAACNNCCTTTCATTTTTTTTTATTGGGGNT  
TNCCNTTATGGN

### Ref 6.1

Sequence of BAC8 using primer C3S7, which spans nucleotides 1513-1532 of the cDNA. Exon sequence is underlined and represents nucleotides 1535-1588.

TTCTTGGGAGCATAGGTGCCAGGCAAGAAATGGTACGGCGAAGCCGAGGACAGCTCG  
GTACGTACACAATAGCTTCTCCTCCTGGTGAGAATTTCTTCAATTTCCCTTGAGTTGTAT  
ATTGTAATGATCATTGTTGCTAGTCTTCAATGTCAATCCTATGCTTTTTAAAAAGTGTTT  
TAAGTGTAACGTGAATTAACCTGAATAATCATTTCTCTGCAGTAATAAAAGTTAGAAT

TCTGATTTAGGTGAGTCA GCATACCGCCCCCCCCCGTTTTCTCTAGAAAGTCTTCTC  
TAGAAAACGTTCTCTAGAAAGTCCTATCTAGAAAACCTTTCTCTAGAAAGTCCTTATGTG  
ATTAATAGCATCCATCCTCCCTTTTTAAATAGACTTTATTTTTGTAGAGCAGTTTTAAGT  
TCACAGCAAAAGTGAGCAAAGGTACAGAGATTTC CATATACCCCTTAGTATGCGTAG  
CCTCCCCCATTATTAACATCCCCCATCAAGAGTAGTGCATTTGTTGTA ACTGGTGAACC  
TACATTAACACATCATCACCCAGAGTCCGCAGTTTACATTAGGGGATCATT CATATAACA  
TCTATTTTTACTTTTTTTTTTTTAGTTGAGACAAGATTCTCGCTCTGTCACCCAAGCTGG  
AGTGCAGTCCGNGTGGATTGTNGGCTTACTGNCN

# Ref 6.2

Sequence of BAC9 using primer C3S7, which spans nucleotides 1513-1532 of the cDNA. Exon sequence is underlined and represents nucleotides 1547-1588.

GTGCCGGCAAGAAATGGTACGGCGAAGCCGAGGACAGCTCGGTACGTACACAATAGC  
TTCTCCTCCTGGTGAGAATTTCTTCAATTTCTTGAGTTGTATATTGTAATGATCATTGT  
TGCTAGTCTTCAATGTCAATCCTATGCTTTTTTAAAAAGTGTTTTAAGTGTA ACTGNGAA  
TTAACTTGAATAATCATTTCTCTGCAGTAATAAAAGTTAGAATTCTGATTTAGGTGAGT  
CAGCATACCGCCCCCCCCCGTTTTCTCTAGAAAGTCTTCTCTAGAAAACGTTCTCTA  
GAAAGTCCTCTCTAGAAAACCTTTCTCTAGAAAGTCCTTATGTGATTAATAGCATCCATC  
CTCCCTTTTTTAAATAAGACTTTATTTTTGTAGAGCAGTTTTAAGTTCACAGCAAAAGTG  
AGCAAAGGGCAGAGATTTC CATATACCCCTTAGTATGCGTAGCCTCCCCCATTATTA  
CATCCCCATCAGAGTAAGNGCATTTGTTGTA ACTGGNGAACCTACAATTNACACATTN  
TNACCCACAGTCCCGCAGGTTTACATTTATGGGATCATTCCCCTANTAACACCTATTT  
TTTTACTTTTTTTTTTTTTTTTAGGTTGAGACAAGAATTTTCGGCTTCTTGTGTACCCCCAA  
ACTNGGTAGTAGNCNNACCGTCGNGNAATTTNTGGGGTTTCNTNGNGNNCANTTTGTG  
CNNTCNNCTTNNCNCNAAAGAANTTTTTTTTACCCTTTTTTTTCCCCCNAANANANN  
ANCCTTCCCCTTGGNGGANGCTGGGGACTTCCNCAGNGGNGG

# Ref 7.1

Sequence of BAC8 using primer C3S8, which spans nucleotides 1842-1860 of the cDNA. Exon sequence is underlined and represents nucleotides 1861-1917.

CAAAGTGCAGTTTATCTCAACACTGTTTTGCTCACAGAGAGCCTTGGTTTCAAAGGTAG  
GTTATTTTGTACCTGCAGTGTTGTCAGACTTTGTTTTTTTTTATTAAACATTGTCTAAGATC  
ATTTGACACATTCATTGGTTAATATATGTAGTAATATATTAATGAATATGTGTAGTTAA  
AATTTAAATAATAACCTAAGACCCTTAATTCTTCTTTGCCTCTCTACTGCTGCCTGCCTT  
TTAGAATTTTTCATTTATTCTGAATCACCTTTAACCAGTTCTGGTTTGAAAAACAGTAAC  
TTGGATGTGGAGAAGGGCCTGAAATTAATAGCCAATCTTAAATATGGGGCTTCTCTTG  
TTTTCTCTTCACTTGGTTCTGTTTTTATAAAAAACTCAATTTATAAAGAATTCAATATAT  
AAGCAATTCAACCCACTGAAATTATTTTATGATGAATGGAAAAGAAGGTATGTGTTTG  
TTCAACTGCTTTAAATGTTTACTTCTTATATTTGTTTTCCCTTAGAAATATGTATATTCTT

AAATTTTGAAGGTAGCTATTTCAATTTAATCATCCTAGAGGATGGAATGCANAGATGTT  
GGATGAAAATAACTTACGTATTATTTTGTAAATAAATATAAGAATTCATATATGGTTGAT  
TACCTAAGTGGTTTTATGCACATTCTGATAGAAAGCTTCACCAACAATCCCTTGNTNGA  
TATATTATTT

### Ref 7.2

Sequence of BAC9 using primer C3S8, which spans nucleotides 1842-1860 of the cDNA. Exon sequence is underlined and represents nucleotides 1864-1917.

AAGTCAGTTTATCTACAACACTGTTTTGCTACACAGAGAGCCTTGGTTTCAAAGGTAGG  
TTATTTTGTACCTGCAGTGTGTCAGACTTTGTTTTTTTTTATTAACATTGTCTAAGATCA  
TTTGACACATTCATTGGTTAATATATGTAGTAATATATTAATGAATATGTGTAGTTAAA  
ATTTAAATAATAACCTAAGACCCTTAATTCTTCTTTGCCTCTCTACTGCTGCCTGCCTTT  
TAGAATTTTTTCATTTATTCGAATCACCTTTAACCAGTTCTGGTTTGAAAAACAGTAACT  
TGGATGTGGAGAAGGGCCTGAAATTAATAGCCAATCTTAAATATGGGGCTTCTCTTGN  
TTTCTCTTCACTTGGTTCTGTTTTTATAAAAACTCAATTTATAAAGAATTCAATATATA  
AGCCATTCACCCACTGAAATTATTTTATGATGAATGGAAAAGAAAGGTATGTGTTTGT  
CACCTGCTTTAAAATGNGACNTCNTAATATTTTGGNTTCCCTTAAGAAAATATGTAT  
AATCCTTAAAANTTTNGAAAGGGANGCTANTTTCATTTTTTNAATCAATCCTAANAGG  
GATTGGGAAATGCNCAAGATTTTTTGATTGAAAAANAACCTTANCGNATTTAATTTTTN  
GGNAATAAAAATAATTAGNAATTCNTATTATGNTTNGAATTACCTAAAGTGGTTTTTAT  
TGCCCCATTTCNTTGATATGNAAAGCCTTTCACCAACCAAAATCCCCNTTGNNAGGAAT  
ATTATTTTTTNANGGGCCTCNTNTTGTGGGGNTGGAAGNAAAAACCTTTGTTCCAAAG  
GGTCCCCNC

### Ref 8.1

Sequence of BAC8 using primer C3S10, which spans nucleotides 2412-2431 of the cDNA. Exon sequence is underlined and represents nucleotides 2432-2523.

AGTGCTAGTCCTCAGCAGCACTTGTTGCTGAATATTTGAGCATGCTGGAGGACCGGAA  
ATATCTTCCTGTGGGATGTGTAACATTTCAAGGTAGGAATCTTCCAGATGTACATTAAAT  
CAAGGTATATCTTTTTTTGGTTTTAGCTTTTCTCACTGGTGTTTAGATTTTTTTAGTTTAT  
AAGGAAAGCTTAAAGACTTAAGCCAATGCTTCACAAGGTGAATTAACATTTACAGTG  
ATTGTCATTAATACATTTTAAAGGAGTACTTCTTGTTGATTCTCTTTCCACAGTTTCTTA  
CCTCTGAATTATCAGCACTATGCTTATTTATTCTCTTTGGCTTTACTGNCTTGNAATCCC  
GTTACATACTTTAACATCTATGGAAATGTATTACTGATAATCAGAATTCAGTAGAAATT  
CTTAATTGGCTTTTACTTCACATAGCAGATATACCAACATTCTCTATTCCCTACATAAA  
ATATTAAGATTATTTTATGACTAATACCCATGACTCACAGATGAGTTTGCCCTCTAGTA  
GGGTCATAATTCTGACCCACTAGTTGAATTCTCTGCTTACCAAGAGNCAGGTATGCTTG  
CTTTTTCTTCAAAACCTGTAAATAGTAGGNTTGGGGATATTNTAAAAATTAGGTAAAT  
GGTATATCTTCTGGTGGAANCAGAAAN

## Ref 8.2

Sequence of BAC9 using primer C3S10, which spans nucleotides 2412-2431 of the cDNA. Exon sequence is underlined and represents nucleotides 2444-2523.

CAGCAGCACTTGTTGCTGAATATTTGAGCATGCTGGAGGACCGGAAATATCTTCCTGT  
GGGATGTGTAACATTTCAGGTAGGAATCTTCCAGATGTACATTAAATCAAGGTATATC  
TTTTTTTGGTTTTAGCTTTTCTCACTGGTGTTTAGATTTTTTTAGTTTATAAGGAAAGCTT  
AAAGACTTAAGCCAATGCTTCACAAGGTGAATTAACATTTCACAGTGATTGTCATTAA  
TACATTTTTTAAGGAGTACTTCTTGTTGATTCTCTTTCCACAGTTTCTTACCTCTGAATTA  
TCAGCACTATGCTTATTTATTCTCTTTGTCTTTACTGCCTTGTAATCCGTTACATACTTT  
AACATCTATGGAAATGTATTACTGATAATCAGAATTCAGTAGAAATTCTTAATTGGCTT  
NTTACTTCACATAGCAGATNTACCAACATTCTCTATTCCCTACATAAAATATTAGGATT  
ATTTTATGACTAATAACCATGACTCACAGATTGAGTTTGCCCTCTANTAGGGTNCATAAT  
TTCTGACCCACTAGTTGAATTCTCTGCTTACCAAAGTCANTTATGCCTTTGCTTTTTCT  
TCAAAACCCTGNTTAATTAGGNACGGCTTTGGAGATAATTTATAAAAAAATTTCAAGCT.  
NAAANTGGNTTATTATTCNTTCCNNGGTTGAAAAAACCCAGGAATTGGCACAAANNA  
NAAAAAGNTTATTCCNNGGTTTCTTTNCGGNAAAAAACCAAAAAATCTTNGAAATTGT  
TTTTTACCAAAAANGACCTCCNCNGGGAAAAAGGGNGTAAATTTNTTCCNTAAAAACN  
N

## Ref 9.1

Sequence of BAC9 using primer C3S11, which spans nucleotides 2679-2698 of the cDNA. Exon sequence is underlined and represents nucleotides 2711-2799.

TTCCTATTCATGAAGCTAATCGGGATGCAAAGAACTATCCACAATTCATGGTAAACT  
TCAAGAAGCATTGAGCAAAATTGTTTCATCAGGTAATGATTCCAATTTCTAGCTTCACTA  
TAAAGGGAAAAAACTGTCTGAAAGCATTAAATGTTGTTTTGCACTGATGTCAAACCTAGA  
TCCCGTGAAATGACCATTTTAATCAGACTACAAATGAGCGGTCAAATGATAGTTCAT  
GGCCAAAGCAAAGCTCATTAAACAATAAAAAATGAATTCACCTAAAGTAAATGGTGATCA  
TCATAAACTTTCTGCATAGCTTTTTTTTTTTTCATTTTTGAATTATTAATTAAGCAAGTTTT  
TAAAAATTGTGATTTTTCTGTTTCACAAGGNAAGATCATAAGTTGNGGAATCTCATTTTT  
AAAAATTGATACCCTATTNCTTTTGCTGNGGAAAANTGGAAGTTTTTTAATATTTTCAA  
GGTTTTTTTTTAAAATTNAAATGGATTGTGGAAAACCTTTTAAATNAATTTAAACCTAC  
CTAAAATANTTTTTTTAATGGNCCNNGCCANCTGGAACCNTTTTATTTTTTTCCCCTAG  
GAATGGTTTTACCCAAATCCATTCCCTTTTGAATAATTTTTTCCCTNAATTNCCCAA  
AAANTTTTTNTTTTTTTGGGNGGAAAAAATANTTGGAAAATTAAAAAAATGGGGGTGG  
GGCCNTAAATGGGGATTATTTTTAAATTTCTAAAAAAGGGANTTTTCCATTACCTTT  
NAATCCTTTTTTGGGNGGNTTCNATTTATTGGGGAATCCTNCNCTTTTTNTNCNCCTTA  
AAAAANTTAGGGCCTNCCAAAATTTTAAACCNTTTAATTTTTNAAAANGGAAAGGGNC  
CCCTTCTTNGCCCGGTTGGTTT



### Ref 10.1

Sequence of BAC8 using primer C3S12, which spans nucleotides 2908-2927 of the cDNA. Exon sequence is underlined and represents nucleotides 2928-2941.

TACAGATTGGAGGTGAATGCTGTGGTGGTTCATAAAATGTCATCTTTAGTTTGTATTCT  
CTCTGATGATTAGACTTTCAGATCCAGATCTAATCATTTAGTAAGCCAGATCTTGCCAA  
ATAAACTACTCCGTTAGAGAATAAGGACTTTTAATAGTTACAATAATACTCTTTCAAAT  
CTTTTATGGCAGCAATAAAATAGTAATATTGTCTATTTTTTTGAGACTATTTTCACACAT  
ATTTTAGAAACCCCTGTATCCTTCAGAATTACTGCGACTTAACGGAGAAATATATAGTA  
TAATCCACATTTTGTGAAAAAGACAAAGAATTAAGTAGTAGCTAATAATTGAACTA  
GAACCAGAACCCTAAGAAATTTCTGACCCAAGCATATTATCTCTTTGGCTTAACCTGGTT  
CCAGGTGAGGTTTCTTTAGAACGTAAAAGCCTGAAATCACACCTTAAAAACACTTCCT  
TTAACCTTTATAATTTCTTAATTTTCACCATAAATGATTGCGTTTTATATTTACTGGGGC  
TAACTAGNATTTTCTGNTATAGGTATTCTTTCCAACCTTTCTCTATTTTTTGTACTCAA  
AGTGTAGTGGATGGACCGGAAGCATTGGGGTTCACCTGGGAGAATGGTTGGNAATGC  
AGAACCCTTAGACCCCAACCCAGCCCCTGTGAAA

### Ref 10.2

Sequence of BAC9 using primer C3S12, which spans nucleotides 2908-2927 of the cDNA. Exon sequence is underlined and represents nucleotides 2930-2941.

CAGATAGTAGGTGAATGCTGTGGTGGTTCATAAAATGTCATCTTTAGTTTGTATTCTCT  
CTGATGATTAGACTTTCAGATCCAGATCTAATCATTTAGTAAGCCAGATCTTGCCAAAT  
AACTACTCCGTTAGAGAATAAGGACTTTTAATAGTTACAATAATACTCTTTCAAATCT  
TTTATGGCAGCAATAAAATAGTAATATTGTCTATTTTTTTGAGACTATTTTCACACATAT  
TTTAGAAACCCCTGTATCCTTCAGAATTACTGCGACTTAACGGAGAAATATATAGTATA  
ATCCACATTTTGTGAAAAAGACAAAGAATTAAGTAGTAGCTAATAATTTGAACTAG  
AACCAGAACCCTAAGAAATTTCTGACCCAAGCATATTATCTCTTTGGCTTAACCTGGTTC  
CAGGNGAGGTATCTTTAGAACGTNAAAGCCTGAAATCACACCTTAAAAACACTTNCTT  
TAACCCTTTATAANTTNCTTAATTTTCACCCATAAAATNGATTGCNGTTTTATATTTTAC  
CTNGGGNCTANACCTNAGGCAATTTTTCTGGGTCATAAGGGGAAATTTCTTTTTCCCAA  
CCCTTTTCTTCTTATTTTGTGTTGGGNCACCTCCCAAAGGTGNTCNGTTGGGGNTTNGGG  
NCCCCGNGAAAGGCCATTTGGGGGNTTCACCCCCGGGGGANGATTTGGTTTTGGAAAA  
TNGTCNNNAAAACCTTCCNNACCCCCNNCCCCCNGGCCCCCNTGNNGGAAATCCAAA  
AGGATCTTGNCNATTTTTTTANCCAAANGANCNCCCCCNAGGGNGGGATTTTNGTTAT  
TTCCCAANAAGANGTAAGGTTNTTGGCCTTTNGGGGCNTTGGGTGTTTTNTTTNN

### Ref 11.1

Bac 9 sequenced with HC3AS3, which spans nucleotides 3376-3393 of the cDNA. Exon sequence is underlined and represents nucleotides 3267-3289.

CTGANGTGTNGCAANGCCACTCCTGTGTCTTTTCTGCATGTCCTCAATAGCAACTTCAA  
TCGGTGTTAAGATGATCTGAGTNANNGAGCATCTGTTANATCAGNGTACTGACTGAAA  
CTATTTAATGAACTTTATGTATAATCAACTGAAATTAGANAAAAAAGATCAATNGT  
AACTTCATGTAAACAATAAAATTCCAACTTGGATTCTAAATGAANNAAAAANATCAA  
CCTTTAAAGAAAAGCTGGGGGTGAATAAGGGCTTAGAAAAGANGTANAAAATGANGA  
CTCAAAATGGTAAAGGGTCTAATATGNATGGATAAGGATGGACATATCTTCGGACTCT  
GAGTGGTGTACATGGCTTGATGATTGCTCACTATGTGTGNCATTATGGCTACCTCTCTT  
TAGGCATGCCTGTTAANTAGGAAGCTGAACTANCAAAGNCTCTTNGATGTATNANTCC  
TGCCGCTNAAGAAGGGGNCGCNTGANNCAAATGATTTGCNATGTNTCTGCTATNATNG  
NAAGNGNTCCTNGANTNNTTCNGANAAANCTCTCNANGAGNCTAGTTTACATNCGGTC  
AGNGCTTCTTGACCTCCTGNGCATCTCCCGTANTTCACCCTCATTNNACCNTNANTTT  
ATAANNANNNAGCCCACTNNCCTATAGGCNATCNACGCNNTTCCCNNTANTCANTNN  
NAGACAATTTTTTNNCGCCCCCTCCTNNTCCTTCCTNNCTTCCNCCCNCCNCCCTNTN  
TCTNTNCCCCCNCCNNTTCTTANCTTNT

#### Ref 12.1

Sequence of BAC9 using primer C3S15, which spans nucleotides 3750-3769 of the cDNA. Exon sequence is underlined and represents nucleotides 3779-4118, and also represent the 3' terminus of the transcriptional unit.

TGTGAAAAGATCTATTGGAAAACAACATGGAATGGAATTCTGGAAATTATTATTNATT  
GAAGAATGCAGTGGCCAAGAAAATATCAAATGTAGATTGTTAACGCTTGAGAATCATG  
GCTATGGTTTCTAATGTTCTGGTAACAAGCTGTTATCTTTTAAGACATTTTAATGACTC  
AAAGGTACACTATACATTTACCATTATTTATACCATAGCTAAGGTAAAAAATTTATTCA  
CTTTAAGTTCGTATTTTTTAATTTATATTACCATTATATAGATTCAATTTGGAACCATTTT  
AAATGTAGTAATGCTTATTTTAAAGGTACTATTAAATATGTGAATGTTTACACTAATTT  
TACCGAGTGGGACTTCAAAATTTTTATTATTGACAATGGCTGAGAACAATTNAAGGGT  
TTGACTCNAGAACTANTTCCAAACCTAGCAGAATAAAAATCATAGATAGCCCCAAATT  
AATGAGTTTGGGNAACTGTNTCAAAGTTTTTTTCCATTTACATACCCAAAAACAGGAA  
ATTTTAGAATTTGCCNGAACCTTTACCTTAAGANAAAAACCCTTTTGTGNTNAAAAATN  
TANTNTTAAAATTCCCGGGGGGANTAATCTTAATNACCCCGGGTGGGGCCANNCNCCC  
CNTTATAACTTTGGAATTTAAAAATTCNTTTTTNTNCAACCCCAAACCTGNANTNGGGT  
NNTTTTNAAGGAAAACCTTTCCACTNGGAAGTTNNCTTTTAGGGNCCNANCCTNCNAN  
AAANNGGGGAANATTGGGAAGTCTTCCCCTTCNTTNGGGGGGNGNCCCAAAAAATTCT  
TAATAAANCCCCGGGGCTCCCATNTTAGNATTTTTTTTTTTGGCCCCACACTGTGTT  
NATTAAANCCCCNCNTGCTAAAAATTTTTNNNGAAAAANACCTNAACCCTTCTNNA

HC2A	-----
KIAA	ASGNLDKNARFS AIYRQDSNKLSNDDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	-----
KIAA	FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLKYDSQ
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	-----VLHHHQNPEFYDEIK
KIAA	KSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVFTRSAFAAVLHHHQNPEFYDEIK
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	IELPTQLHEKHLLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
KIAA	IELPTQLHEKHLLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTODQHLHNFFQYC
KIAA	PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTODQHLHNFFQYC
rat	-----
HC4	-----
HC1	-----
HC3	-----GPGPARSTVVISLISNSARV
HC5	-----
HC2A	OKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
KIAA	OKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
rat	-----
HC4	-----MEIQVLIRFLSVILMQLFWVLPNMIHEDDVPI SCPMV
HC1	-----MSFLPIILNQLFKVLV-QNEEDEITTTVTRV
HC3	NRSRSLSNSNPDISGTPTSPDDEVRSIIGSKGLDRSNSWVNTGGPKAAPWGSNPSPSAES
HC5	-----

HC2A I I H V V A Q C H E E G L E S H L R S Y V K Y A Y K A E P Y V A S E Y K T V H E E L T K S M T T I L K P S A D F L T S N  
KIAA I I H V V A Q C H E E G L E S H L R S Y V K Y A Y K A E P Y V A S E Y K T V H E E L T K S M T T I L K P S A D F L T S N  
rat -----  
HC4 L F H I V S K C H E E G L D S Y L S S F I K Y S F R P G K P S A P Q A P L I H E T L A T M M I A L L K Q S A D F L A I N  
HC1 L P D I V A K C H E E Q L D H S V Q S Y I K F V F K T R --- A C K E R P V H E D L A K N V T G L L K - S N D S P T V K  
HC3 T Q A M D R S C N R M S S H T E T S S F L Q T L T G R L P --- T K K L F H E E L A L Q W V V C S G -- S V R --- E  
HC5 -----

Cadherin  
Cleavage

HC2A K L L R Y S W F F F D V L I K S M A Q H L I E N S K V K L I R N Q R F P A S Y H H A A E T V V N M L M P H I T Q K F G D  
KIAA K L L K Y S W F F F D V L I K S M A Q H L I E N S K V K L I R N Q R F P A S Y H H A V E T V V N M L M P H I T Q K F R D  
rat -----  
HC4 K L L K Y S W F F F E I I A K S M A T Y L L E E N K I K L T H G Q R F P K A Y H H A L H S L F L A I T - I V E S Q Y A E  
HC1 H V L K H S W F F F A I I L K S M A Q H L I D T N K I Q L E R P Q R F P E S Y Q N E L D N L V M V L S D H V I W K Y K D  
HC3 S A L Q Q A W F F F E L M V K S M V H H L Y F N D K L E A P R K S R F P E R F M D D I A A L V S T I A S D I V S R F Q K  
HC5 -----

1.1/1.2/2.1/2.2

HC2A N P E A S K N A N H S L A V F I K R C F T F M D R G F V F K Q I N --- N Y I S -- C F A P G D E K T L F E Y K F E F L  
KIAA N P E A S K N A N H S L A V F I K R C F T F M D R G F V F K Q I N --- N Y I S -- C F A P G D P K T L F E Y K F E F L  
rat -----  
HC4 I P K E S R N V N Y S L A S F L K C C L T I M D R G F V F N L I N --- D Y I S -- G F S P K D P K V L A E Y K F E F L  
HC1 A L E E T R R A T H S V A R F L K R C F T F M D R G C V F K M V N --- N Y I S -- M F S S G D L K T L C Q Y K F D F L  
HC3 D T E M V E R L N T S L A F F L N D L L S V M D R G F V F S L I K S C Y K Q V S S K L Y S L P N P S V I V S L R L D F L  
HC5 -----

3.1/3.2

HC2A R V V C N H E H Y I P L N L P M --- P F G K G R I Q R --- Y Q D L Q L --- D Y S L T D E F  
KIAA R V V C N H E H Y I P L N L P M --- P F G K G R I Q R --- Y Q D L Q L --- D Y S L T D E F  
rat -----  
HC4 Q T I C N H E H Y I P L N L P M --- A F A K P K L Q R --- V Q D S N L --- E Y S L S E Y  
HC1 Q E V C Q E H F I P L C L P I R S A N I P D P L T P S E S --- T Q E L H A S D M P E Y S V T N E F  
HC3 R I I C S H E H Y V T L N L P C S L L T P P A S P S P S V S S A T S Q S S G F S T N V Q D Q K I A N M F E L S -- V P F  
HC5 ----- M N A D T A P T S P C P S I S --- S Q N S S S C S S F Q D Q K I A S M F D R T S R V P A

4.1/4.2

Cadherin  
EC motif

HC2A C R N H F L V G L L L R E V G T A L Q E F R E --- V R L I A I S V L K N L L I K H S F D D R Y A S R S H Q A R I A T  
KIAA C R N H F L V G L L L R E V G T A L Q E F R E --- V R L I A I S V L K N L L I K H S F D D R Y A S R S H Q A R I A T  
rat -----  
HC4 C K H H F L V G L L L R E T S I A L Q D N Y E --- I R Y T A I S V I K N L L I K H A F D T R Y Q H K N Q Q A K I A Q  
HC1 C R K H F L I G I L L R E V G F A L Q E D Q D --- V R H L A L A V L K N L M A K H S F D D R Y R E P R K Q A Q I A S  
HC3 R Q Q H Y L A G I V L T E L A V I L D P D A E G L F G L H K K V I N M V H N L L S S H D S D P R Y S D P Q I K A R V A M  
HC5 S S T S - S P G L F T E L A A A L D A E G E G I S E V Q R K A V S A I H S L L S S H D L D P R C V K P E V K V K I A A

HC2A L Y L P L F G L L I E N V Q R I N V R D V S P F P V N A G - M T V K D E S L A L P A V N P L V T P Q K G S T L D N S L H  
KIAA L Y L P L F G L L I E N V Q R I N V R D V S P F P V N A G - M T V K D E S L A L P A V N P L V T P Q K G S T L D N S L H  
rat -----  
HC4 L Y L P F V G L L L E N I Q R L A G R D T L Y S C A M P N S A S R D E F P C G --- F T S P -- A N -- R G S L S  
HC1 L Y M P L Y G M L L D N M P R I Y L K D L Y P F T V N T S N Q G S R D D L S T N G G F Q S Q T A I K H A N S V D T S F S  
HC3 L Y L P L I G I I M E T V P Q L Y D F T E T H N Q R G R P I C I A T D D Y E S E --- S G --- S M I S  
HC5 L Y L P L V G I I L D A L P Q L C D F T V A D T R R Y R --- T S G S D E E Q E --- G A --- G A I T



HC2A KDLLGAISGIAEPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQSS  
 KIAA KDLLGAISGIAEPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQSS  
 rat -----  
 HC4 TDKDTAYGSFQNG-----HGKREDSRGSLIP-EGATGFPDQGNLTGEN-----TRQS  
 HC1 KDVLNSIAAFSS-----IAISTVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPL  
 HC3 QTVAMAIAGTSVPQ-----LTRPGSFLLTSTSGRQHT-----  
 HC5 QNVALAIAGNNFN-----LKTSG-IVLSSLPYKQYN-----

5.1/5.2

HC2A TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSDDALFTYWN-KASTSELMDFFTISEVCL  
 KIAA TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSDDALFTYWN-KASTSELMDFFTISEVCL  
 rat -----  
 HC4 STRSSVSQYNRLDQYEIRSLLMCYLYIVKMISEDTLTYWN-KVSPQELINILILLEVCL  
 HC1 ALIGSTLRFDRLDQAETRSLLMCFHIMKTISYETLIAYWQ-RAPSPEVSDFFSIIDVCL  
 HC3 -----TFSAESSRSLICLLWVLKN-ADETVLQKWFTDLSVLQLNRLDLLLYLCV  
 HC5 -----MLNADTTRNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRILDLLFICV

HC2A HQFYMGKRYIARNQEGLG--PIVHDRKS-----QTLPVSRNRTGMM  
 KIAA HQFYMGKRYIAR-----TGM  
 rat -----  
 HC4 FHFYMGKRNIA RVHDAWLSKHFGIDRKS-----QTMPALNRSGVM  
 HC1 QNFRYLGKRNIIRKIAAAF--KFVQSTQWNGTLKGSNPSCQTSGLLAQNMHSTSRHEGKH  
 HC3 SCFEYKGGKVFERMNSLTFK--KSKDMRAK-----LEEAILGSI GARQEMV  
 HC5 LCFEYKGGKQSSDKVSTQVLQ--KSRDVKAR-----LEEALLRGE GARGEMM

HC2A HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC  
 KIAA HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC  
 rat -----  
 HC4 QARLQHL-----SSLESS-----FTLNHSSTTTEADI FHQALLEGNTATEVS  
 HC1 QHRSQTLPIIRGK--NALSNPKL----LQMLDNTMTSNEIDIVHHVDTEANIATEGC  
 HC3 RRSRGQLERSPSGSAFGSQENLRWRKDMTHWRONTEKLDKSRAEIEHEALIDGNLATEAN  
 HC5 RRRAPGNDRFP-----GLNENLRWKKEQTHWRQANEKLDKTKAELDQEALISGNLATEAH

6.1/6.2

HC2A LTALDTLSLFTLAFNQLLADHGHNPMLKKVFDVYLCFLQKHQSE TALKNVFTALRSLIY  
 KIAA LTALDTLSLFTLAFNQLLADHGHNPMLKKVFDVYLCFLQKHQSE TALKNVFTALRSLIY  
 rat -----KLSRGHSPMLKKVFDVYLCFLQKHQSE MALKNVFTALRSLIY  
 HC4 LTVLDTISFFTQCFKTHFLNNDGHNPMLKKVFDIHLAFLKNGQSEVSLKHVFASLRAFIS  
 HC1 LTILDLVSLFTQTHQRQLQQCDQNSLMKRGFDTYMLFFQVNOQSATALKHVFASLRLFVC  
 HC3 LIILDTLEIVVQTVS--VTES--KESILGGVLKVLLHSMACNQSAVYLQHC FATQALVS  
 HC5 LIILDMQENIIQASS--ALDC--KDSLLGGVLRVLVNSLNCQSTTYLTHCFATLALIA

HC2A KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTH  
 KIAA KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTH  
 rat KFPSTFYEGRADMCASLCYEVLKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTH  
 HC4 KFPSAFFKGRVNMCAAFCEYVLKCCCTSKISSTRNEASALLYLIMRNNEFYTKRKTFLRTH  
 HC1 KFPSAFFQGPADLCGSFCYEVLKCCNHRSRSTQTEASALLYLIMRNNEFENKQKSIVRSH  
 HC3 KFPPELLFEEETEQCADLCLRLLRHCSSSIGTIRSHPSASLYLLMRQNF EIGN--NFARVK  
 HC5 KFGDLLFEEVEEQCFDLCHQVLHHCSSSMDVTRSQACATLYLLMRFSFGATS--NFARVK

7.1/7.2

HC2A LQVIISVSQLIADVVGIGETRFOQSLSIINNCANS DRLIKHTSFSSDVKD LTKRIRTVLM  
 KIAA LQVIISVSQLIADVVGIGETRFOQSLSIINNCANS DRLIKHTSFSSDVKD LTKRIRTVLM  
 rat LQVIISLSQLIADVVGIGETRFOQSLSIINNCANS DRLIKHTSFSSDVKD LTKRIRTVLM  
 HC4 LQIIIAVSQLIADVALSGGSRFQESLFIINN FANS DRPMLARAFPAEVKD LTKRIRTVLM  
 HC1 LQLIKAVSQLIAD-AGIGGSRFQHS LAITNNFANGDKQMN FNPPAEVKD LTKRIRTVLM  
 HC3 MQVPMSLSSLVGTSQNFEEFLRRSLKTI LTYAEEDLELRETTFPDQVQDLVFNLMHILS  
 HC5 MQVTMSLASLVGRAPDFNEEHLRRSLRTI LAYSEEDTAMQMPPTQVEELLCNLNSILY

Refs

		Transmembrane
HC2A	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD	SMARIHVKNGLSEAAMCYVHV
KIAA	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD	SMARIHVKNGLSEAAMCYVHV
rat	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD	SMARIHVKNGLSEAAMCYVHV
HC4	ATAQMKEHEKDPEMLIDLQYSLAKSYASTPELRKTWLD	SMARIHVKNGLFSEAAMCYVHV
HC1	ATAQMKEHEKDPEMLVDLQYSLANSYASTPELRRTWLE	SMARIHVKNGLSEAAMCYVHV
HC3	DTVCMKEHQEDPEMLIDLMYRIAKGYQTS	PDLRLTLQNMAGKHSERSNHAEEAAQCLVHS
HC5	DTVCMREFQEDPEMLMDLMYRIAKSYQAS	PDLRLTLQNMAGKHTKKKCYTEAAMCLVHA

	domain	SH3	
HC2A	TALVAEYITRKGV		FRQGCTAFRVITPN
KIAA	TALVAEYITRKEA	VQWEPPLLPHSHSACLRRSRGGVFRQGCTAFRVITPN	
rat	TALVAEYITRKEAD	LALQREPPVFPYSHTSCQRKSRGGMFRQGCTAFRVITPN	
HC4	AALVAEYITRKKL		FPNGCSAFKKITPN
HC1	AALIAEYITRKGYWKVEKIG	ASLLSEDPCHPCDSNSLLTTFSGGSMFSGMWP	AFSLITPN
HC3	AALVAEYITRLED		RKYLPGVCVTFQNISSN
HC5	AALVAEYITRLED		HSYLPVGSVSFQNISSN

8.1/8.2

		ITAM
HC2A	IDEEASMMEDVGMQD	VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIPI
KIAA	IDEEASMMEDVGMQD	VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIPI
rat	IDEEASMMEDVGMQD	VHFNEDVLMELLEQCADGLWKAERLRAGLLTSINSSSP
HC4	IDEEGAMKEDAGMMD	VHYSEEVLMELLEQCENGLWKAERYEISEISKLIPI
HC1	IKEEGAAKEDSGMHD	TPYNEINILVEQLYMCGEFLWKSEYELIADVKNKPIIAV
HC3	VLEESAVSDDVVS	PDEEGICSGKYFTESGLVGLLEQAAASF
HC5	VLEESVVS	EDTLSPDEGVCAGQYFTESGLVGLLEQAAELFSTGGLYETVNEWYKLVIP

	ITAM	ITAM	ITAM	ITAM
HC2A	YEKRRD			
KIAA	YEKRRD	FERLAHLDTTHRAYSKYTEVMHSGRLLGTYFRVAFFGQAAQYQFTDSETDVE		
rat	SMKSGGTLETTHLYDTTHRAYSKYTEVITR		A	AGSWDLLPGGLFGQ
HC4	YENRREFENLTQVYRTIHGAYTKILEVMHTKKRLG			TFFRVAFYGQ
HC1	FEKQDFKFLSDLYDYDHRSYLKVAEVNSEKRLFG			FYYRVAFYGQ
HC3	HEANRDAKKLSTIHGKLQEA	FSKIVHSTGWERMFG		TYFRVGFYF
HC5	LEAHREFRKLTLTHSKLQRA	FDSIVNKDH--KRMFG		TYFRVGFYF

9.1

	ITAM	ITAM
HC2A	-FFEDEDGKEYIYKEPKLTPLSEISORLLKIYSDHFGSENVKMIQDSGKVNPKDLDSKHA	
KIAA	GFFEDEDGKEYIYKEPKLTPLSEISORLLKIYSDHFGSENVKMIQDSGKVNPKDLDSKHA	
rat	GFFEDEDGKEYIYKEPKLTPLSEISORLLKIYSDHFGSENVKMIQDSGKVNPKDLDSKHA	
HC4	SFFEDEDGKEYIYKEPKLTGLSEISLRLVKIYGEHFGTENVKIIQDSKVNNAKELDPKHA	
HC1	GFFEDEDGKEYIYKEPKLTGLSEISORLLKIYADHFGADNVKIIQDSKVNNAKELDPKHA	
HC3	TKFGDLDEQEFVYKEPAITKLAEISHRLGEYGERFGEDVVEVIKDSNPVDKCKLDPNKA	
HC5	SKFGDLDEQEFVYKEPAITKLPEISHRLGEYGERFGEDVVEVIKDSNPVDKCKLDPNKA	

10.1/10.2

	ITAM
HC2A	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
KIAA	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
rat	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
HC4	HIQVTYVKPYFDDKELTERKTEFERNHNISRFVFEAPYTLGKKGCCIEEQCKRRTILT
HC1	YIQVTYVTPFFDEKEIEDRKTDFEMHHNINRFVFETPFTLSGKKHGGVAEQCKRRTILT
HC3	YIQVTYVTPFFDEKEIEDRKTDFEMHHNINRFVFETPFTLSGKKHGGVAEQCKRRTILT
HC5	YIQVTYVTPFFDEKEIEDRKTDFEMHHNINRFVFETPFTLSGKKHGGVAEQCKRRTILT

Coiled-Coil 1

HC2A	I H C F P Y V K K R I P V M Y Q H H T D L N H I E V A I D E M S K K V A E L R Q L C S S A E V D M I K L Q L K L Q G S V	
KIAA	I H C F P Y V K K R I P V M Y Q H H T D L N H I E V A I D E M S K K V A E L R Q L C S S A E V D M I K L Q L K L Q G S V	
rat	I H C F P Y V K K R I P V M Y Q H H T D L N H I E V A I D E M S K K V A E L H Q L C S S A E V D M I K L Q L K L Q G S V	
HC4	S N S F P Y V K K R I P I N C E Q Q I N L K R I D G A T D E I K D K T A E L Q K L C S S T D V D M I Q L Q L K L Q G W V	
HC1	S H L F P Y V K K R I Q V I S Q S S T E L N H I E V A I D E M S R K V S E L N Q L C T M E E V D M I S L Q L K L Q G S V	
HC3	S H A F P Y I K T R V N V T H K E I I L T R I E V A I E D M Q K K T Q E L A F A T H Q D P A D P K M L Q M V L Q G S V	11.1
HC5	M H A F P Y I K T R I S V I Q K E E F V L T R I E V A I E D M K K K T L Q L A V A I N Q E P P D A K M L Q M V L Q G S V	

Coiled-Coil 2

HC2A	S V Q V N A G P L A Y A R A F L D D T N T K R Y P D N K V K L L K E V F R Q F V E A C G Q A L A V N E R L I K E D Q L E
KIAA	S V Q V N A G P L A Y A R A F L D D T N T K R Y P D N K V K L L K E V F R Q F V E A C G Q A L A V N E R L I K E D Q L E
rat	S V Q V N A G P L A Y A R A F L D D T N T K R Y P D N K V K L L K E V F R Q F V E A C G Q A L A V N E R L I K E D Q L E
HC4	S V Q V N A G P L A Y A R A F L N D S Q A S K Y P P K K V S E L K D M F R K F I Q A C S I A L E L N E R L I K E D Q V E
HC1	S V K V N A G P M A Y A R A F L E E T N A K K Y P D N Q V K L L K E I F R Q F A D A C G Q A L D V N E R L I K E D Q L E
HC3	G T T V N Q G P L E V A Q V F L S E I P S D P K L F R H H N K L R L C F K D F T K R C E D A L R K N K S L I G P V Q K E
HC5	G A T V N Q G P L E V A Q V F L A E I P A D P K L Y R H H N K L R L C F K E F I M R C G E A V E K N K R L I T A D Q R E

Coiled-Coil 2

HC2A	Y Q E E M K A N Y R E M A K E L S E I M H E Q I C P L E E K T S - V L P N S L H I F N A I S G T P T S T M V H G M T S S
KIAA	Y Q E E M K A N Y R E M A K E L S E I M H E Q L G - - - - -
rat	Y Q E E M K A N Y R E I R K E L S D I I V E R I C P G E D K R A T K F P A H L Q R H Q R D T N K H S G S R V D Q F I L S
HC4	Y H E G L K S N F R D M V K E L S D I I H E Q I L Q E D T M H S P W M S N T L H V F C A I S G T S S D R G Y G S P R Y A
HC1	Y Q E E L R S H Y K D M L S E L S T V M N E Q I T G R D D L S K - - - R G V D Q T C T R V I S K A T P A L P T V S I S S
HC3	Y Q R E L G - - - - K L S S - - - - - P Z - - - - -
HC5	Y Q Q E L K K N Y N K L K E N L R P M I E R K I P E L Y K P I F R V E S Q K R D S F H R S S F R K C E T Q L S Q G S Z -

PBM

HC2A	S S V V Z - - - - -
KIAA	- - - - -
rat	C V T L P H E P H V G T C F V M C K L R T T F R A N H W F C Q A Q E E A M G N G R E K E P W T V I F N S R F Y R S W G K
HC4	E V Z - - - - -
HC1	S A E V Z - - - - -
HC3	- - - - -
HC5	- - - - -

HC2A	- - - - -
KIAA	- - - - -
rat	V H I F F
HC4	- - - - -
HC1	- - - - -
HC3	- - - - -
HC5	- - - - -

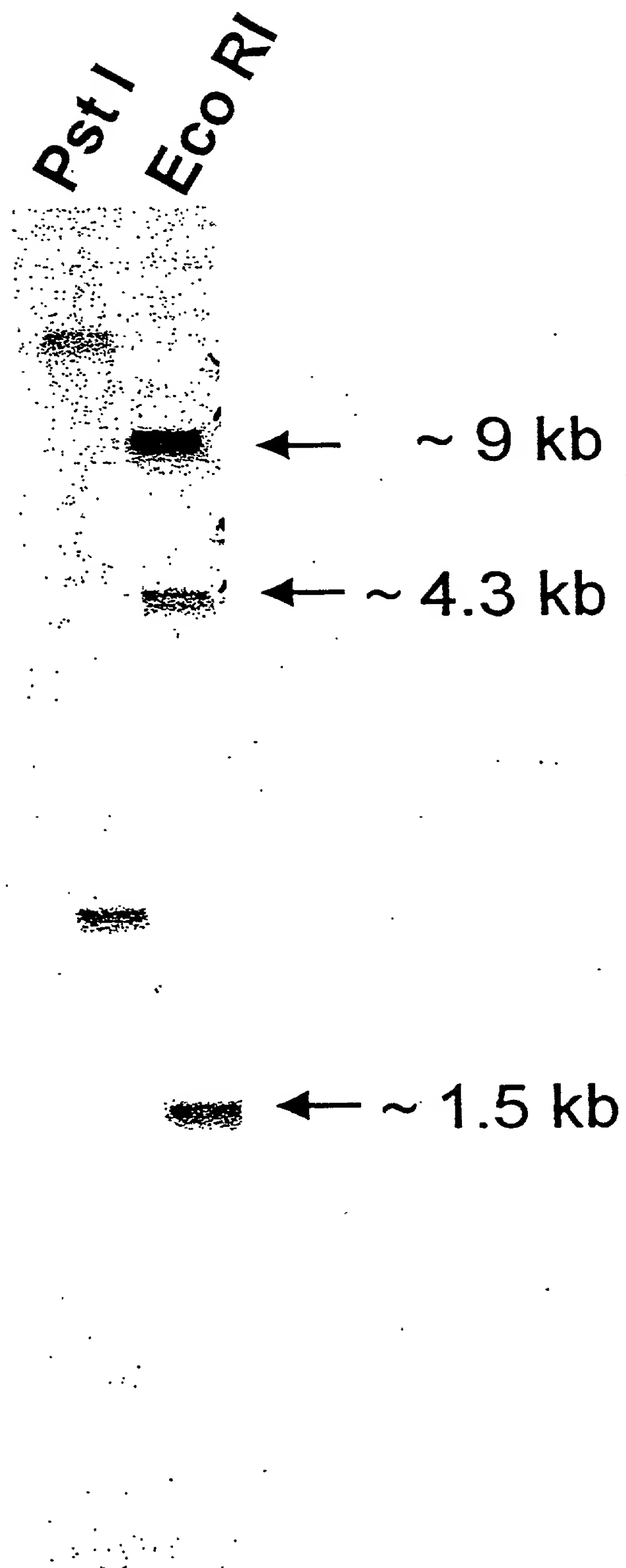
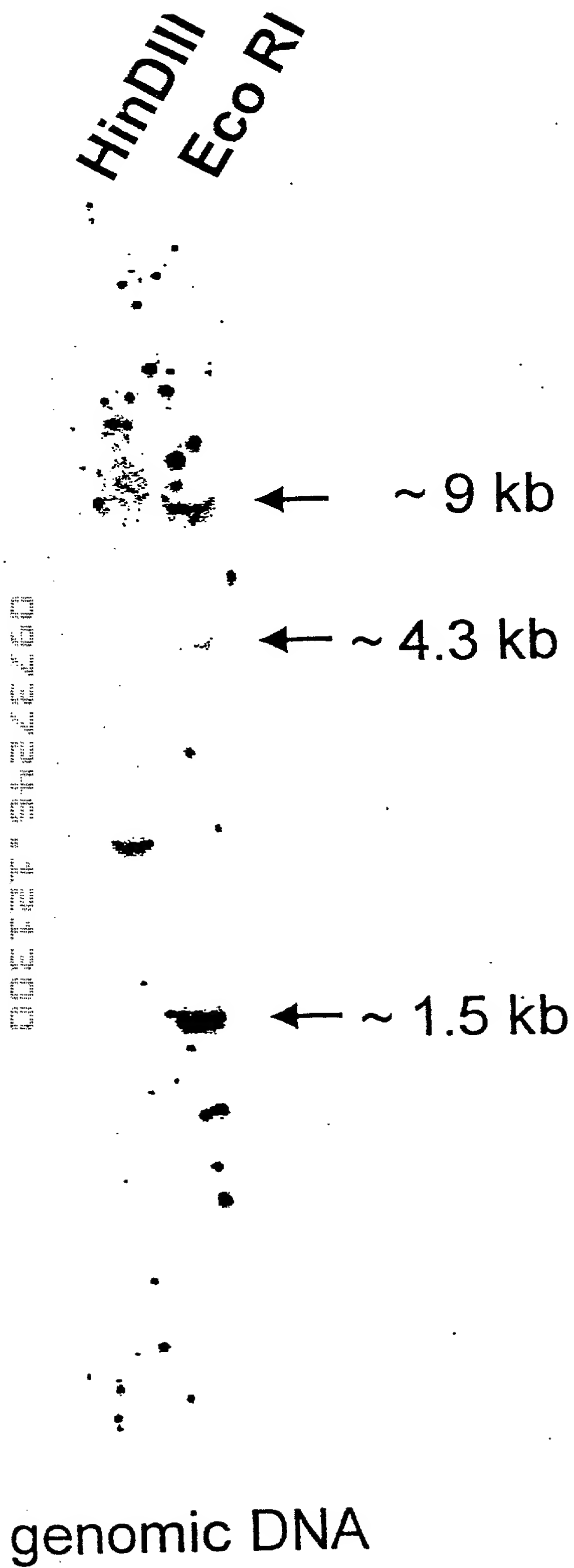


FIG. 5

GTCGCCGTCGCCGCAGCAGCC -1

1/1	ATG GCC GAG CGC CGC GCC TTC GCC CAG AAG	31/11	ATC AGC AGA ACG GTG GCA GCC GAA GTT AGG
Met ala glu arg arg ala phe ala gln lys	61/21	91/31	ile ser arg thr val ala ala glu val arg
AAG CAG ATC TCC GGA CAA TAT AGT GGT TCT	121/41	151/51	CCC CAA CTG CTC AAA AAC CTT AAT ATT GTT
lys gln ile ser gly gln tyr ser gly ser	181/61	211/71	pro gln leu leu lys asn leu asn ile val
GGC AAT ATA TCC CAT CAC ACC ACA GTG CCC	241/81	271/91	CTT ACC GAA GCA GTA GAT CCA GTG GAT TTG
gly asn ile ser his his thr thr val pro	301/101	331/111	leu thr glu ala val asp pro val asp leu
GAA GAT TAC CTC ATT ACT CAT CCT TTG GCT	361/121	391/131	GTG GAT TCT GGG CCT TTA CGG GAT TTG ATT
glu asp tyr leu ile thr his pro leu ala	421/141	451/151	val asp ser gly pro leu arg asp leu ile
GAA TTT CCT CCA GAT GAT ATT GAA GTT GTT	481/161	511/171	TAT AGT CCT CGG GAC TGC AGA ACT CTT GTT
glu phe pro pro asp asp ile glu val val	541/181	571/191	tyr ser pro arg asp cys arg thr leu val
TCA GCT GTA CCT GAA GAA AGT GAA ATG GAT	601/201	631/211	CCA CAT GTT AGA GAC TGT ATA AGA AGT TAT
ser ala val pro glu glu ser glu met asp	661/221	691/231	pro his val arg asp cys ile arg ser tyr
ACA GAA GAC TGG GCA ATT GTC ATC AGA AAA	721/241	751/251	TAT CAT AAA TTG GGA ACA GGA TTT AAT CCC
thr glu asp trp ala ile val ile arg lys	781/261	811/271	tyr his lys leu gly thr gly phe asn pro
AAT ACA TTA GAT AAA CAG AAA GAA AGG CAA	841/281	871/291	AAA GGT TTG CCA AAA CAA GTT TTT GAA TCT
asn thr leu asp lys gln lys glu arg gln	901/301	931/311	lys gly leu pro lys gln val phe glu ser
GAT GAA GCT CCA GAT GGC AAC AGC TAC CAG	961/321	991/331	GAT GAT CAA GAT GAC CTT AAA AGA CGT TCA
asp glu ala pro asp gly asn ser tyr gln			asp asp gln asp asp leu lys arg arg ser
ATG TCA ATA GAT GAT ACC CCA AGG GGT AGC			TGG GCC TGT AGT ATC TTT GAC TTG AAA AAT
met ser ile asp asp thr pro arg gly ser			trp ala cys ser ile phe asp leu lys asn
TCA CTT CCT GAT GCT TTG CTT CCC AAT TTA			CTT GAT CGA ACT CCA AAT GAA GAA ATA GAC
ser leu pro asp ala leu leu pro asn leu			leu asp arg thr pro asn glu glu ile asp
CGT CAG AAT GAT GAC CAA AGG AAA TCA AAC			CGT CAC AAA GAA CTT TTT GCT TTG CAT CCA
arg gln asn asp asp gln arg lys ser asn			arg his lys glu leu phe ala leu his pro
TCA CCA GAT GAG GAA GAA CCA ATA GAA CGG			CTT AGT GTT CCT GAT ATA CCC AAA GAA CAT
ser pro asp glu glu glu pro ile glu arg			leu ser val pro asp ile pro lys glu his
TTT GGT CAA AGA CTT CTT GTA AAA TGC TTA			TCA CTC AAG TTT GAA ATT GAA ATT GAA CCC
phe gly gln arg leu leu val lys cys leu			ser leu lys phe glu ile glu ile glu pro
ATT TTT GCA AGT TTG GCT TTA TAT GAT GTC			AAG GAA AAG AAA AAG ATT TCA GAA AAC TTT
ile phe ala ser leu ala leu tyr asp val			lys glu lys lys lys ile ser glu asn phe
TAT TTT GAC CTT AAT TCT GAG CAG ATG AAA			GGG TTG TTA CGT CCA CAT GTA CCA CCT GCT
tyr phe asp leu asn ser glu gln met lys			gly leu leu arg pro his val pro pro ala
GCC ATT ACT ACC CTG GCA AGA TCA GCA ATT			TTT TCT ATC ACT TAT CCT TCC CAA GAT GTT
ala ile thr thr leu ala arg ser ala ile			phe ser ile thr tyr pro ser gln asp val



1021/341	1051/351
TTT CTT GTA ATA AAG CTA GAA AAA GTC CTA	CAG CAA GGA GAC ATT GGA GAG TGT GCA GAA
phe leu val ile lys leu glu lys val leu	gln gln gly asp ile gly glu cys ala glu
1081/361	1111/371
CCA TAT ATG ATT TTC AAA GAA GCA GAT GCC	ACC AAG AAT AAA GAA AAA CTG GAG AAA CTG
pro tyr met ile phe lys glu ala asp ala	thr lys asn lys glu lys leu glu lys leu
1141/381	1171/391
AAG AGT CAA GCA GAT CAG TTT TGC CAA AGA	CTT GGG AAA TAT CGC ATG CCT TTT GCT TGG
lys ser gln ala asp gln phe cys gln arg	leu gly lys tyr arg met pro phe ala trp
1201/401	1231/411
ACT GCA ATC CAT TTA ATG AAT ATT GTT AGC	AGT GCT GGG AGT TTG GAA AGA GAT TCT ACA
thr ala ile his leu met asn ile val ser	ser ala gly ser leu glu arg asp ser thr
1261/421	1291/431
GAA GTA GAA ATC AGT ACT GGA GAA CGA AAA	GGG TCT TGG TCA GAG AGG AGG AAT TCT AGT
glu val glu ile ser thr gly glu arg lys	gly ser trp ser glu arg arg asn ser ser
1321/441	1351/451
ATT GTT GGC AGA CGA TCA CTT GAA AGG ACA	ACA AGT GGA GAT GAT GCT TGT AAC TTG ACG
ile val gly arg arg ser leu glu arg thr	thr ser gly asp asp ala cys asn leu thr
1381/461	1411/471
AGC TTT CGA CCA GCT ACT CTC ACA GTG ACA	AAT TTT TTT AAG CAG GAA GGA GAC CGC TTA
ser phe arg pro ala thr leu thr val thr	asn phe phe lys gln glu gly asp arg leu
1441/481	1471/491
AGT GAT GAA GAT CTC TAC AAA TTC CTT GCT	GAT ATG AGA AGG CCA TCT TCT GTC TTA CGG
ser asp glu asp leu tyr lys phe leu ala	asp met arg arg pro ser ser val leu arg
1501/501	1531/511
CGA CTA AGA CCT ATT ACA GCT CAG CTC AAG	ATA GAC ATT TCT CCC GCA CCT GAA AAT CCC
arg leu arg pro ile thr ala gln leu lys	ile asp ile ser pro ala pro glu asn pro
1561/521	1591/531
CAT TAT TGC CTA ACT CCG GAG CTG CTT CAA	GTG AAG CTT TAC CCT GAC AGT AGA GTT AGA
his tyr cys leu thr pro glu leu leu gln	val lys leu tyr pro asp ser arg val arg
1621/541	1651/551
CCT ACC AGA GAA ATC TTA GAG TTT CCC GCA	AGG GAT GTT TAT GTT CCA AAC ACT ACT TAC
pro thr arg glu ile leu glu phe pro ala	arg asp val tyr val pro asn thr thr tyr
1681/561	1711/571
AGA AAT CTT CTC TAC ATA TAC CCT CAG AGT	CTT AAT TTT GCC AAT CGT CAA GGT TCT GCT
arg asn leu leu tyr ile tyr pro gln ser	leu asn phe ala asn arg gln gly ser ala
1741/581	1771/591
AGA AAT ATA ACA GTG AAA GTC CAG TTT ATG	TAT GGA GAG GAT CCA AGC AAT GCC ATG CCG
arg asn ile thr val lys val gln phe met	tyr gly glu asp pro ser asn ala met pro
1801/601	1831/611
GTA ATC TTT GGT AAA TCT AGC TGT TCA GAA	TTT TCA AAG GAA GCC TAT ACA GCC GTA GTA
val ile phe gly lys ser ser cys ser glu	phe ser lys glu ala tyr thr ala val val
1861/621	1891/631
TAT CAT AAC AGG TCT CCT GAT TTT CAT GAA	GAA ATC AAG GTT AAG CTT CCT GCT ACT TTA
tyr his asn arg ser pro asp phe his glu	glu ile lys val lys leu pro ala thr leu
1921/641	1951/651
ACT GAC CAT CAT CAC TTG CTT TTT ACT TTT	TAT CAT GTT AGT TGT CAA CAA AAA CAA AAT
thr asp his his his leu leu phe thr phe	tyr his val ser cys gln gln lys gln asn
1981/661	2011/671
ACT CCT CTT GAA ACA CCA GTT GGA TAT ACA	TGG ATA CCA ATG CTT CAG AAT GGA CGG TTG
thr pro leu glu thr pro val gly tyr thr	trp ile pro met leu gln asn gly arg leu
2041/681	2071/691
AAG ACT GGC CAG TTT TGC TTG CCA GTC TCA	TTG GAA AAA CCA CCA CAG GCT TAT TCT GTA
lys thr gly gln phe cys leu pro val ser	leu glu lys pro pro gln ala tyr ser val
2101/701	2131/711
CTG TCT CCT GAG GTT CCT CTA CCT GGC ATG	AAA TGG GTA GAT AAT CAC AAA GGT GTT TTT
leu ser pro glu val pro leu pro gly met	lys trp val asp asn his lys gly val phe



3301/1101	GTG TCT TCA AAG CTT TAC TCA TTA CCG AAT	3331/1111	CCC AGT GTT CTG GTG TCC TTG AGG CTG GAT
val ser ser lys leu tyr ser leu pro asn		pro ser val leu val ser leu arg leu asp	
3361/1121	TTT CTA CGA ATC ATC TGC AGT CAT GAG CAC	3391/1131	TAT GTT ACA TTA AAC TTA CCC TGC AGC TTA
phe leu arg ile ile cys ser his glu his		tyr val thr leu asn leu pro cys ser leu	
3421/1141	CTT ACT CCA CCT GCA TCT CCA TCA CCT TCT	3451/1151	GTT TCT TCT GCA ACA TCT CAG AGT TCT GGA
leu thr pro pro ala ser pro ser pro ser		val ser ser ala thr ser gln ser ser gly	
3481/1161	TTT TCT ACG AAT GTA CAA GAC CAA AAG ATT	3511/1171	GCA AAT ATG TTT GAA TTA TCC GTG CCT TTC
phe ser thr asn val gln asp gln lys ile		ala asn met phe glu leu ser val pro phe	
3541/1181	CGC CAA CAG CAT TAT TTG GCA GGA CTT GTG	3571/1191	TTA ACA GAG CTG GCT GTC ATT TTA GAC CCT
arg gln gln his tyr leu ala gly leu val		leu thr glu leu ala val ile leu asp pro	
3601/1201	GAT GCT GAA GGA CTG TTT GGA TTG CAT AAG	3631/1211	AAA GTC ATC AAT ATG GTA CAC AAT TTA CTC
asp ala glu gly leu phe gly leu his lys		lys val ile asn met val his asn leu leu	
3661/1221	TCC AGT CAC GAC TCA GAC CCG CGG TAC TCT	3691/1231	GAC CCT CAG ATA AAG GCT CGA GTG GCC ATG
ser ser his asp ser asp pro arg tyr ser		asp pro gln ile lys ala arg val ala met	
3721/1241	TTG TAT CTA CCT CTG ATT GGT ATT ATC ATG	3751/1251	GAA ACT GTA CCT CAG CTG TAT GAT TTT ACA
leu tyr leu pro leu ile gly ile ile met		glu thr val pro gln leu tyr asp phe thr	
3781/1261	GAA ACT CAC AAT CAA CGA GGA AGA CCA ATT	3811/1271	TGT ATA GCC ACT GAT GAT TAT GAA AGT GAG
glu thr his asn gln arg gly arg pro ile		cys ile ala thr asp asp tyr glu ser glu	
3841/1281	AGC GGA AGT ATG ATA AGC CAG ACC GTT GCC	3871/1291	ATG GCA ATC GCA GGG ACA TCG GTC CCT CAA
ser gly ser met ile ser gln thr val ala		met ala ile ala gly thr ser val pro gln	
3901/1301	CTA ACA AGG CCT GGC AGT TTC CTC CTC ACG	3931/1311	TCA ACG AGT GGC AGG CAA CAC ACT ACC TTT
leu thr arg pro gly ser phe leu leu thr		ser thr ser gly arg gln his thr thr phe	
3961/1321	TCA GCA GAA TCA AGT CGA AGC CTT TTG ATC	3991/1331	TGT CTA CTT TGG GTT CTC AAA AAT GCA GAT
ser ala glu ser ser arg ser leu leu ile		cys leu leu trp val leu lys asn ala asp	
4021/1341	GAA ACA GTT CTA CAG AAG TGG TTT ACA GAT	4051/1351	CTC TCA GTC TTG CAG CTA AAC CGG CTA TTA
glu thr val leu gln lys trp phe thr asp		leu ser val leu gln leu asn arg leu leu	
4081/1361	GAT CTG CTT TAT CTC TGT GTG TCT TGC TTT	4111/1371	GAG TAT AAA GGG AAA AAA GTG TTT GAA CGA
asp leu leu tyr leu cys val ser cys phe		glu tyr lys gly lys lys val phe glu arg	
4141/1381	ATG AAT AGC TTG ACC TTT AAG AAA TCA AAA	4171/1391	GAC ATG AGA GCA AAG CTT GAA GAA GCT ATT
met asn ser leu thr phe lys lys ser lys		asp met arg ala lys leu glu glu ala ile	
4201/1401	CTT GGG AGC ATA GGT GCC AGG CAA GAA ATG	4231/1411	GTA CGG CGA AGC CGA GGA CAG CTC GAG AGA
leu gly ser ile gly ala arg gln glu met		val arg arg ser arg gly gln leu glu arg	
4261/1421	AGC CCA TCT GGA AGT GCC TTT GGA AGT CAA	4291/1431	GAA AAT TTG AGG TGG AGG AAA GAT ATG ACT
ser pro ser gly ser ala phe gly ser gln		glu asn leu arg trp arg lys asp met thr	
4321/1441	CAC TGG CGT CAA AAC ACA GAG AAG CTT GAC	4351/1451	AAA TCA AGA GCA GAG ATT GAA CAC GAA GCA
his trp arg gln asn thr glu lys leu asp		lys ser arg ala glu ile glu his glu ala	
4381/1461	CTG ATT GAT GGA AAC CTG GCT ACA GAA GCA	4411/1471	AAC CTA ATC ATT TTA GAT ACA TTA GAG ATT
leu ile asp gly asn leu ala thr glu ala		asn leu ile ile leu asp thr leu glu ile	



4441/1481	4471/1491
GTT GTT CAG ACC GTT TCT GTA ACG GAA TCC	AAA GAG AGC ATT CTT GGT GGA GTG CTA AAA
val val gln thr val ser val thr glu ser	lys glu ser ile leu gly gly val leu lys
4501/1501	4531/1511
GTG CTA CTA CAC AGC ATG GCC TGT AAC CAA	AGT GCA GTT TAT CTA CAA CAC TGT TTT GCT
val leu leu his ser met ala cys asn gln	ser ala val tyr leu gln his cys phe ala
4561/1521	4591/1531
ACA CAG AGA GCC TTG GTT TCA AAG TTT CCT	GAA CTC TTA TTT GAA GAA GAG ACA GAG CAG
thr gln arg ala leu val ser lys phe pro	glu leu leu phe glu glu glu thr glu gln
4621/1541	4651/1551
TGT GCT GAT TTA TGC CTC AGG CTT CTC CGA	CAC TGT AGC AGT AGC ATC GGT ACA ATA CGG
cys ala asp leu cys leu arg leu leu arg	his cys ser ser ser ile gly thr ile arg
4681/1561	4711/1571
TCA CAC CCC AGT GCC TCC CTT TAC CTA CTA	ATG AGG CAA AAC TTT GAG ATT GGG AAT AAC
ser his pro ser ala ser leu tyr leu leu	met arg gln asn phe glu ile gly asn asn
4741/1581	4771/1591
TTT GCC AGG GTT AAA ATG CAG GTA CCA ATG	TCA CTA TCC TCC TTG GTG GGC ACA TCT CAG
phe ala arg val lys met gln val pro met	ser leu ser ser leu val gly thr ser gln
4801/1601	4831/1611
AAT TTT AAT GAA GAA TTC TTA AGA CGT TCT	CTA AAG ACT ATA TTG ACA TAT GCT GAA GAA
asn phe asn glu glu phe leu arg arg ser	leu lys thr ile leu thr tyr ala glu glu
4861/1621	4891/1631
GAT CTG GAA TTG AGG GAA ACA ACA TTT CCT	GAT CAG GTC CAG GAT CTG GTT TTC AAT CTC
asp leu glu leu arg glu thr thr phe pro	asp gln val gln asp leu val phe asn leu
4921/1641	4951/1651
CAT ATG ATT CTT TCT GAT ACT GTG AAA ATG	AAG GAA CAC CAG GAG GAT CCT GAA ATG TTG
his met ile leu ser asp thr val lys met	lys glu his gln glu asp pro glu met leu
4981/1661	5011/1671
ATT GAT CTA ATG TAC AGA ATT GCC AAG GGT	TAC CAG ACC TCT CCA GAG CGA TTG ACC TGG
ile asp leu met tyr arg ile ala lys gly	tyr gln thr ser pro glu arg leu thr trp
5041/1681	5071/1691
TTG CAG AAC ATG GCA GGC AAG CAC TCA GAA	CGA AGC AAT CAT GCT GAA GCT GCA CAG TGT
leu gln asn met ala gly lys his ser glu	arg ser asn his ala glu ala ala gln cys
5101/1701	5131/1711
CTA GTC CAC TCA GCA GCA CTT GTT GCT GAA	TAT TTG AGC ATG CTG GAG GAC CGG AAA TAT
leu val his ser ala ala leu val ala glu	tyr leu ser met leu glu asp arg lys tyr
5161/1721	5191/1731
CTT CCT GTG GGA TGT GTA ACA TTT CAG AAT	ATT TCA TCT AAT GTT TTA GAA GAA TCT GCG
leu pro val gly cys val thr phe gln asn	ile ser ser asn val leu glu glu ser ala
5221/1741	5251/1751
GTC TCA GAT GAT GTG GTA TCT CCA GAT GAA	GAA GGT ATC TGC TCT GGA AAA TAC TTT ACT
val ser asp asp val val ser pro asp glu	glu gly ile cys ser gly lys tyr phe thr
5281/1761	5311/1771
GAG TCA GGA CTT GTG GGA TTA CTG GAA CAA	GCA GCT GCT TCC TTC TCT ATG GCT GGC ATG
glu ser gly leu val gly leu leu glu gln	ala ala ala ser phe ser met ala gly met
5341/1781	5371/1791
TAT GAA GCA GTT AAT GAA GTT TAC AAA GTA	CTT ATT CCT ATT CAT GAA GCT AAT CGG GAT
tyr glu ala val asn glu val tyr lys val	leu ile pro ile his glu ala asn arg asp
5401/1801	5431/1811
GCA AAG AAA CTA TCC ACA ATT CAT GGT AAA	CTT CAA GAA GCA TTC AGC AAA ATT GTT CAT
ala lys lys leu ser thr ile his gly lys	leu gln glu ala phe ser lys ile val his
5461/1821	5491/1831
CAG AGT ACT GGC TGG GAG CGG ATG TTT GGC	ACC TAT TTT CGT GTT GGT TTT TAT GGA ACC
gln ser thr gly trp glu arg met phe gly	thr tyr phe arg val gly phe tyr gly thr
5521/1841	5551/1851
AAG TTC GGG GAT TTG GAT GAA CAA GAA TTT	GTT TAC AAG GAG CCT GCA ATA ACC AAA CTT
lys phe gly asp leu asp glu gln glu phe	val tyr lys glu pro ala ile thr lys leu

5581/1861	5611/1871
GCA GAG ATA TCT CAC AGA TTG GAG GGA TTT	TAC GGA GAA AGA TTT GGA GAG GAT GTG GTT
ala glu ile ser his arg leu glu gly phe	tyr gly glu arg phe gly glu asp val val
5641/1881	5671/1891
GAA GTA ATC AAA GAC TCT AAT CCT GTA GAC	AAG TGT AAA TTA GAT CCT AAC AAG GCA TAT
glu val ile lys asp ser asn pro val asp	lys cys lys leu asp pro asn lys ala tyr
5701/1901	5731/1911
ATT CAG ATT ACC TAT GTG GAG CCA TAC TTT	GAC ACA TAT GAG ATG AAG GAC AGA ATC ACC
ile gln ile thr tyr val glu pro tyr phe	asp thr tyr glu met lys asp arg ile thr
5761/1921	5791/1931
TAT TTC GAC AAA AAT TAC AAT CTT CGT CGA	TTC ATG TAC TGT ACA CCC TTT ACT TTA GAT
tyr phe asp lys asn tyr asn leu arg arg	phe met tyr cys thr pro phe thr leu asp
5821/1941	5851/1951
GGC CGT GCC CAT GGG GAA CTT CAT GAA CAA	TTC AAA AGG AAG ACC ATT CTG ACT ACG TCT
gly arg ala his gly glu leu his glu gln	phe lys arg lys thr ile leu thr thr ser
5881/1961	5911/1971
CAT GCC TTT CCT TAT ATT AAA ACA AGG GTC	AAT GTC ACT CAT AAA GAA GAG ATC ATC TTA
his ala phe pro tyr ile lys thr arg val	asn val thr his lys glu glu ile ile leu
5941/1981	5971/1991
ACA CCA ATT GAA GTT GCT ATT GAG GAC ATG	CAG AAA AAG ACA CAG GAG TTG GCA TTT GCA
thr pro ile glu val ala ile glu asp met	gln lys lys thr gln glu leu ala phe ala
6001/2001	6031/2011
ACA CAT CAG GAT CCC GCA GAC CCC AAA ATG	CTT CAG ATG GTA CTC CAG GGA TCT GTA GGC
thr his gln asp pro ala asp pro lys met	leu gln met val leu gln gly ser val gly
6061/2021	6091/2031
ACC ACA GTG AAT CAG GGG CCT TTG GAA GTT	GCC CAG GTT TTT CTG TCT GAA ATA CCT AGT
thr thr val asn gln gly pro leu glu val	ala gln val phe leu ser glu ile pro ser
6121/2041	6151/2051
GAC CCA AAG CTC TTC AGA CAT CAT AAT AAA	CTG CGA CTC TGC TTT AAA GAT TTT ACT AAA
asp pro lys leu phe arg his his asn lys	leu arg leu cys phe lys asp phe thr lys
6181/2061	6211/2071
AGG TGT GAA GAT GCC TTA AGA AAA AAT AAG	AGC TTA ATT GGG CCG GTT CAA AAG GAG TAT
arg cys glu asp ala leu arg lys asn lys	ser leu ile gly pro val gln lys glu tyr
6241/2081	6271/2091
CAA AGG GAA TTG GGG AAA CTA TCT TCG CCT TAA	
gln arg glu leu gly lys leu ser ser pro OCH	

AGAGGCCCTACAGCCCTAGATCACAGAAAGTCCCTCAGTTATCCAAGCCAGTATTGCTTGTCCCCTGCCACAGAGATTCC  
 TTCAGTCGAATGAGCTTTCGCAAAATGGATCTCTAAACTGAATGCACTTGTTTTATTTCATCTGCAAAGAGCCATGTATTC  
 AACATCGAGTGTGAAAAGATCTATTGGAAACCAACATGGAATGGAATTCTGGAAATTATTATTTCATTGAAGAATGCAGTG  
 GCCAAGAAAATATCAAATGTAGATTGTTAACGCTTGAGAATCATGGCTATGGTTTCTAATGTTTCGGGTAACAAGCTGTTA  
 TCTTTTAAGACATTTTAAATGACTCAAAGGTACACTATACATTTACCATTATTTATACCATAGCTAAGGTTAAAAATTTAT  
 TCACTTTAAGTTCGTATTTTTTAATTTATATCACCATTTATAGATTCATTTTGGACCCATTTTAAATGTAGTAATGCTTA  
 TTTTAAAGGTACTAAAAATATGTGAATGTTTACCTCGTGCGGCCAGGGCCTC

A. Allelic Variations: single nucleotide changes (polymorphisms) between hCLASP-3 cDNAs and/or genomic sequences

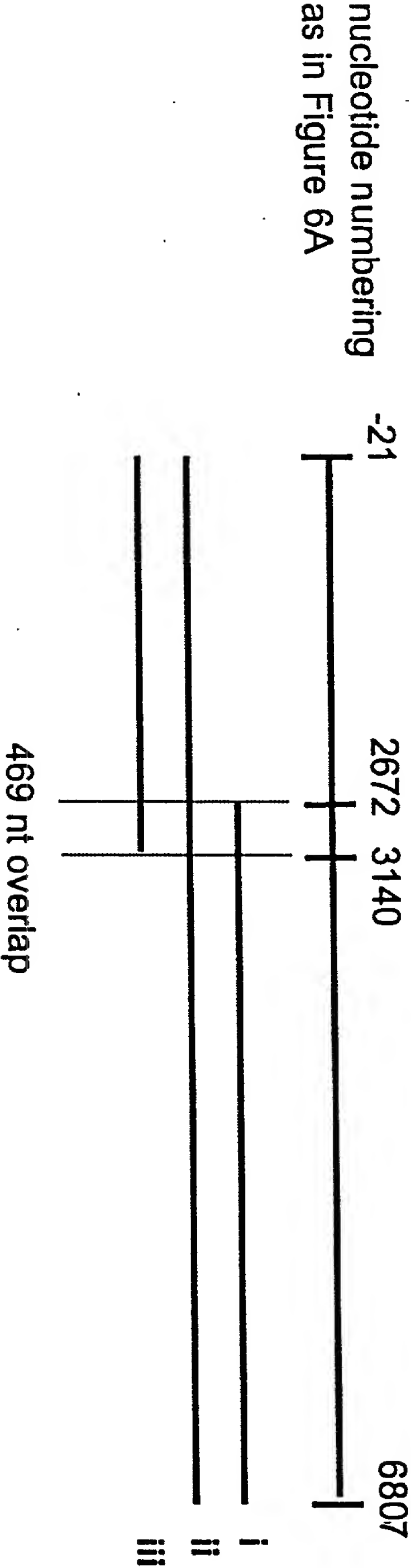
Isoform	Difference	Nucleotide position	Consequence
1	polymorphism	318	A to G; missense
2	polymorphism	323	A to G; Glu to Gly
3	polymorphism	2187	T to C; missense
4	polymorphism	3165	T to G; Asp to Glu

B. Alternative Exon usage

Isoform	Difference	Nucleotide position	Consequence
1	Exon deletion	2768-2860, inclusive	In frame deletion – 33 amino acids removed

These differences may be found separately or together in various combinations in the different human CLASP-3 isoforms

FIG. 6



C

FIG. 6A

Exon 60270 - 20370

CGCCGCAGCCGCCGCCGCCGTCGCCGTCGCCGCAGCAGCCATGGCCGAGCGC  
CGCGCCTTCGCCCAGAAGATCAGCAGGTAAATATCCGGCGTGCGGCGC

Exon 85360 - 85510

GTTTTTGCTTTCTTCATTGTAGAACGGTGGCAGCCGAAGTTAGGAAGCAGATC  
TCCGGACAATATAGTGGTTCTCCCCAACTGCTCAAAAACCTTAATATTGTTGG  
CAATATATCCCATCACACCACAGTAAGTAACGTATTCAAAATATA

Exon 94500 - 94720

TCTTATCCCAACTTTTTACAAAGGTGCCCCCTTACCGAAGCAGTAGATCCAGTG  
GATTTGGAAGATTACCTCATTACTCATCCTTTGGCTGTGGATTCTGGGCCTTT  
ACGGGATTTGATTGAATTCCTCCAGATGATATTGAAGTTGTTTATAGTCCTC  
GGGACTGCAGAACTCTTGTTTCAGCTGTACCTGAAGAAAGGTAAGGAGACAT  
TGACTTATT

Exon 94870 - 94980

TATTTTCCTTTTTTAAAATAGTGAAATGGATCCACATGTTAGAGACTGTATAAG  
AAGTTATACAGAAGACTGGGCAATTGTCATCAGAAAGTAAGTTATATGTTTA  
TTACAA

Exon 100110 - 100290

ATTTATTTAACTTTTTTTCTTTAATAGATATCATAAATTGGGAACAGGATTAA  
TCCCAATACATTAGATAAACAGAAAGAAAGGCAAAAAGGTTTGCCAAAACA  
AGTTTTTGAATCTGATGAAGCTCCAGATGGCAACAGCTACCAGGATGATCAA  
GTAATACTTTTATTCTTAAATAA

Exon 100340 - 100600

ATATTTAATGTTTTGTCATGACAGGATGACCTTAAAAGACGTTCAATGTCAATA  
GATGATACCCCAAGGGGTAGCTGGGCCTGTAGTATCTTTGACTTGAAAAATT  
CACTTCCTGATGCTTTGCTTCCCAATTTACTTGATCGAACTCCAAATGAAGAA  
ATAGACCGTCAGAATGATGACCAAAGGAAATCAAACCGTCACAAAGAACTTI  
TTGCTTTGTCATCCATCACCAGATGAGGTATAGATGTTTGCATATAAAGAA



Exon 100880-101020

TTTTGGTGTTGCTTTTCAATTTGTAGGAAGAACCAATAGAACGGCTTAGTGTT  
CCTGATATACCCAAAGAACATTTTGGTCAAAGACTTCTTGTAATGCTTATC  
ACTCAAGTGAGTATTTATTTCTTTTACTTACAAC

Exon 112010 – 112120

TTTTTCTTCATAAAGGTTTGAAATTGAAATTGAACCCATTTTGGCAAGTTTGG  
CTTTATATGATGTCAAGGAAAAGAAAAAGGTAAGATTATATAATTTGACCAT  
AGTTAT

Exon 113680 – 113880

AAGTTTAACATACTAATATTTTTTAGATTTTCAGAAAACTTTATTTTGACCTTA  
ATTCTGAGCAGATGAAAGGGTTGTTACGTCCACATGTACCACCTGCTGCCATT  
ACTACCCTGGCAAGATCAGCAATTTTTCTATCACTTATCCTTCCCAAGATGT  
TTTTCTTGTAATAAAGGTGAGAATAATGTTAAATATATTG

Exon 115020-115160

TTAATCTTAACTTTTTTGCCTTTGACAGCTAGAAAAAGTCCTACAGCAAGGA  
GACATTGGAGAGTGTGCAGAACCATATATGATTTTCAAAGAAGCAGATGCCA  
CCAAGGTAGAATGTTATGCTTCTCATTTCCGCCAC

Exon 117200 – 117410

ATGTATAAAGTTCTGTTTTGCAGAATAAAGAAAAACTGGAGAACTGAAGAG  
TCAAGCAGATCAGTTTTGCCAAAGACTTGGGAAATATCGCATGCCTTTTGCTT  
GGACTGCAATCCATTTAATGAATATTGTTAGCAGTGCTGGGAGTTTGGAAAG  
AGATTCTACAGAAGTAGAAATCAGTACTGGAGGTAAGAGTGTTTCATACAAA  
AC

Exon 123200 - 123396

AAAATGAATTTTTTTTTTAATTCTTTGTAGAACGAAAAGGGTCTTGGTCAGA  
GAGGAGGAATTCTAGTATTGTTGGCAGACGATCACTTGAAAGGACAACAAGT  
GGAGATGATGCTTGTAACCTTGACGAGCTTTCGACCAGCTACTCTCACAGTGAC  
AAATTTTTTAAAGCAGGTATTGTTCTGTCATGTAGGAATTT

(Next part of CLASP, starting

GAAGGAGACCGCTTAAGTGATGAAGATCTCTACAAATTCCTTGCTGATATGA  
GAAGGCCATCTTCTGTCTTACGGCGACTAAGACCTATTACAG)

Exon 5560 – 5710

CTTTTTCCTCTATTATTGAAATCAGGAAGGAGACCGCTTAAGTGATGAAGATC  
TCTACAAATTCCTTGCTGATATGAGAAGGCCATCTTCTGTCTTACGGCGACTA  
AGACCTATTACAGGTATTTAAAAATTTTGAGTAGAAATGGTTGCA

Exon 6680-6900

TTACATTGTTTTTTAATATATAATTTGCAGCTCAGCTCAAGATAGACATTCTC  
CCGCACCTGAAAATCCCCATTATTGCCTAACTCCGGAGCTGCTTCAAGTGAA  
GCTTTACCCTGACAGTAGAGTTAGACCTACCAGAGAAATCTTAGAGTTTCCCG  
CAAGGGATGTTTATGTTCCAAACACTACTTACAGGTAAGAGATTTTAATTGG  
AGAATTCTG

Exon 38920 – 39075

GTATTTACTATCATCTATACTGTTGCTTTCACAGAAATCTTCTCTACATATACC  
CTCAGAGTCTTAATTTTGCCAATCGTCAAGGTTCTGCTAGAAATATAACAGTG  
AAAGTCCAGTTTATGTATGGAGAGGATCCAAGCAATGCCATGCCGGTAA



hCLASP4	-----MFPMEDISISVIGRQRRTVQ-----	20
hCLASP5	-----MTHLNSLDVQLAQELG-----	16
hCLASP3	-----MAERRAFAQKISRTVAAEVRKQISGQYSGSPQLLKNLNIVG	41
hCLASP2	-----MLLFPYDDFQTAILRRQGRYICS-----	23
hCLASP7	-----MAASERRAFAHKINRTVAAEVRKQVSRERSGSPHSSRRCSSSL	43
hCLASP1	MSFRGKVFVKREPSEFWKKRRTVRRVIQEEFHRFSSQEKPRLLEPLDYETVIEELEKTYRN	60
...:		
hCLASP4	-----STVPEDAEKRAQSLFVKECIKTYSTDWHVNVNYK	53
hCLASP5	-----DFT	19
hCLASP3	N-----ISHHTTVPLTEAVDPVDLEDYLITHPLAVDSGPLRDLIEFP	83
hCLASP2	-----TVPKAEAAAQSLFVTECIKTYNSDWHLVNYK	55
hCLASP7	G-----VPLTEVVEPLDFEDVLLSRPPDAEPGPLRDLVEFP	79
hCLASP1	DPLQDLLFFPSDDFSAATVSWDIRTLYSTVPEDAEHKAENLLVKEACKFYSSQWHVNVNYK	120
::		
hCLASP4	YEDFSGDFRMLPCKSLRPEKIPNHVFEIDEDCEKDED-----SSSLCSQKGGVIKQG	105
hCLASP5	DDDLDVVFTPKCRTLQP-SLPEEGVELDPHVR-----DCVQTYIREWLI	63
hCLASP3	PDDIEVVYSPRDCRTLVS-AVPEE-SEMDPHVR-----DCIRSYTEDWAI	126
hCLASP2	YEDYSGEFRQLPNKVVKLDKLPVHVYEVDEEVDKDED-----AASLGSQKGGITKHG	107
hCLASP7	ADDLELLLQPRECRTEP-GIPKD-EKLDAQVR-----AAVEMYIEDWVI	122
hCLASP1	YEQYSGDIRQLPRAEYKPEKLPSHSFEIDHEDADKDEDTTSHSSSKGGGGAGGTGVFKSG	180
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hCLASP4	WLHKANVNSTIT--VTMKVFKRRYFYLTQLPDGSIYILNSYKDEKNSKESK-GCIYLDACI	162
hCLASP5	VNRKNQGSPEIC--GFKKTGSRKDFHKT-LPKQTFESETLECSEPAQA--GPRHLNVLC	118
hCLASP3	VIRKYHKLGTGF--NPNTLDKQKERQKG-LPKQVFESDEAPDGNSYQDDQDDLKRRSMI	183
hCLASP2	WLYKGNMNSAIS--VTMRSFKRRFFHLIQLGDGSIYILNSYKDEKISKEPK-GSIFLDSCM	164
hCLASP7	VHRRYQYLSAAY--SPVTTDTQORERQKG-LPRQVFQDASGDERSGPEDSNDSTRGSGSP	179
hCLASP1	WLYKGNFNSTVNNTVTVRSFKKRYFQLTQLPDNSYIMNFYKDEKISKEPK-GCIFLDSC	239
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hCLASP4	DVVQCPKMRRHAFELKMLDKYSHYLAETEQUEMEEWLITLKKIIQINTDSLVOEKKETVE	222
hCLASP5	DVSGKGPVTACDFDLRSLQPDKRLLENLLOQVSAEDFEKQNEEARRTN-----ROAE	169
hCLASP3	DDTPRGSWACSI FDLKNSLPDALLPNLLDRTPNEEIDRQNDQQRKSN-----RHKE	234
hCLASP2	GVVQNNKVRRAFELKMQDKSSYLLAADSEVEMEEWITILNKILQLN-----FEAAMQEK	219
hCLASP7	EDTPRSSGASSI FDLRNLAADSLPSLLERAAPEDVDRRNETLRRQH-----RPPA	230
hCLASP1	GVVQNNRLRKYAFELKMNDLTYFVLAAETESDMDEWIHTLNRILQISPEGPLQGRSTEL	299
* : * : : : :		
hCLASP4	TAQDDDETSS----QGKAENIMASLERSMHPELMKYGRETEQLNKLRSRGDGRQNLFSFDSE	278
hCLASP5	LFALYPSVD----EEDAVEIRPVPECPKEHLG-----N-----RILVKLLTLKFEIE	212
hCLASP3	LFALHPSPD----EEPIERLSVPDIPKEHFG-----QRLLVKCLSLKFEIE	277
hCLASP2	RNGDSHEDD----EQSKLEGSGSGLDSYLP ELAKSAREAEIK---LKSESRVKLFYLDPD	272
hCLASP7	LLTLYPAPD----EDEAVERCSRPEPPREHFG-----QRLVKCLSLKFEIE	273
hCLASP1	TDLGLDSL DNSVTCECTPEETDSS ENNLHADFAKYLTETEDTVKTTNRNRLNLFSLDPD	359
: : : : :		
hCLASP4	VQRLDFS----GIEPDIKP-FEEKCNKRFLVNCHDLTFNILGQIGDNAKGPPTNVEPFFI	333
hCLASP5	IEPLFAS----IALYDVKERKKISENFHCDLNSDQFKGFLRAHTPSVAASSQARS AVFSV	268
hCLASP3	IEPIFAS----LALYDVKEKKKISENFYFDLNS EQMKGLLRPHVPPAAITTLARSAIFSI	333
hCLASP2	AQKLDFS----SAEPEVKS-FEEKFGKRILVKCNDLSFNLOCCVAENEEGPTTNVEPFFV	327
hCLASP7	IEPIFGI----LALYDVREKKKISENFYFDLNSDSMKGLLRAGHThPAISTLARSAIFSV	329
hCLASP1	IDTLKLQKKDLLEPESVIKPFEEKAAKRIMIICKALNSNLQGCVTENENDPITNIEPFFV	419
: : : : : : : : * :		

hCLASP4	NLALFDVKNCKISADFHVDLNPPSVREMLWGSSTQLASDGSP---	KGSSPESYIHGIAE	390
hCLASP5	TYPSSDIYLVVKIEKVLQOQD----	IGDCAEPYTVIKESDG-----GKSKE-KIEKLKL	317
hCLASP3	TYPQDVFLVIKLEKVLQOQD----	IGECAEPYMI FKEADA-----TKNKE-KLEKLKS	382
hCLASP2	TLSLFDIKYNRKISADFHVDLNHFSVRQMLATTSPALMNGS-----	GQSPSVLKGILHE	381
hCLASP7	TYPSPDIFLVIKLEKVLQOQD----	ISECCEPYMVLKEVDT-----AKNKE-KLEKLRL	378
hCLASP1	SVALYDLRDSRKISADFHVDLNHAAVRQMLLGASVALENGNIDTITPRQSEEPHIKGLPE		479
	. . * : * : . : . : . . . . :		
hCLASP4	SQLRYIQQGI FSVTNPHPEIFLVARIEKVLQGNITHCAEPYIKNSDPVKTAQKVHRTAKQ		450
hCLASP5	QAESFCQR-----LGKYRMPFAWAPISLSSFFNVSTLEREVDVDSVVGSRSPVGERRTLA		372
hCLASP3	QADQFCQR-----LGKYRMPFAWTAIHLMNIVSSAGSLERDSTEVEISTGERKGSWSERR		437
hCLASP2	AAMQYPKQGI FSVTCPPHDI FLVARIEKVLQGSITHCAEPYMKSSDSSKVAQKVLKNAKQ		441
hCLASP7	AAEQFCTR-----LGRYRMPFAWTAVHLANIVSSAGQLDRDSD----	SEGERRPAWTDRR	429
hCLASP1	EWLKFPPKQAVFSVSNPHSEIVLVAKIEKVLGMNIGASGAEPYIKNPDSNKYAQKILKSNRQ		539
	: : : . : : . . :		
hCLASP4	VCSRLGQYRMPFAWAARPI FKDTQGSLLDGRFSPLYKQDSSKLSSEDIKLLSEYKKPE		510
hCLASP5	QSRRLSERALSLEENGVGSNFKTS-----TLSSVSSFFKQEGDRLSDEDLFKFLADYKRSS		427
hCLASP3	NSSI VGRRLERTTSGDDACNLTSFR-PATLTVTNFFKQEGDRLSDEDLYKFLADMRRPS		496
hCLASP2	ACQRLGQYRMPFAWAARTLFKDASGNLDKNARFSAIYRQDSNKLSDNDMLKLLADFRKPE		501
hCLASP7	---RRGPQ--DRASSGDDACSFSGFR-PATLTVTNFFKQEAERLSDEDLFKFLADMRRPS		483
hCLASP1	FCSKLGKYRRAFAWAVRSVFKDNQGNVDRDSRFSPLFRQESSKISTEDLVKLVSDYRRAD		599
	. . : : : : : * : * : * : : : . . . .		
hCLASP4	--KTKLQIIPGQLNITVECVVDLSNCITSSYVPLKPFE-KNCQNTVEVEEFVPEMTKY		567
hCLASP5	SLQRRVKSIPGLLRLEISTAPEIINCCLTPEMLPVKPPF-ENRTRPHKEILEFP--TREV		484
hCLASP3	SVLRRRLRPITAQLKIDISPAPENPHYCLTPELLQVKLYP-DSRVRPTREILEFP--ARDV		553
hCLASP2	K-MAKLPVILGNLDITIDNVSSDFPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKH		560
hCLASP7	SLLRRLRPVTAQLKIDISPAPENPHFCLSPELLHIKPYP-DPRGRPTKEILEFP--AREV		540
hCLASP1	R-ISKMQTIPGSLDIAVDNVPLEHPNCVTSSFIPVKPFNMMAQTEPTVEVEEFVYDSTKY		658
	: : . . * : : . . . . : : * : : * : *		
hCLASP4	CYPFTIYKNHLYVYPLQLKYDSQKTFAKARNIAVCVEFRDSDSDASALKCIYGKPAAGSV		627
hCLASP5	YVPHTVYRNLLYVYPQRLNFVN--KLASARNITIKIQFMCG-EDASNAMPVIFGKSSGPE		541
hCLASP3	YVPNTTYRNLLYIYPQSLNFAN--RQGSARNITVKVQFMYG-EDPSNAMPVIFGKSSCSE		610
hCLASP2	TQPYTIYTNHLYVYPKYLYKYSQKSFARKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPV		620
hCLASP7	YAPHTSYRNLLYVYPHSLNFSS--RQGSVRNLAVRVQYMTG-EDPSQALPVIFGKSSCSE		597
hCLASP1	CRPYRVYKNQIYIYPKHLKYDSQKCFNKARNITVCIEFKNSDEESAKPLKCIYGKPEGPL		718
	* * * : : * * : : . . * : : : : : . * . . . : * : * .		
hCLASP4	FTTNAYAVVSHHNQNPFEFYDEIKIELPIHLHQKHLLFTFYHVSCBINTKGTTKKQDTVE		687
hCLASP5	FLQBVYTAVTYHNKSPDFYEEVKIKLPAKLTNVHLLFTFYHISCOQ-----KQASVE		595
hCLASP3	FSKEAYTAVVYHNRSPDFHEEIKVKLPATLTDHLLFTFYHVSCQ-----KQNTLE		664
hCLASP2	FTRSAFAAVLHHHQNPEFYDEIKIELPTQLHEKHLLLTFFHVSCDNSSKGSTKKRDVE		680
hCLASP7	FTRBAFTPVVYHNKSPDFYEEFKLHLPACVTENHLLFTFYHVSCOP-----RPGTALE		651
hCLASP1	FTSAAYTAVLHHSQNPDFSDEVKIELPTQLHEKHILFSFYHVTCIDINAKANAKKKEALE		778
	* . . : * : * : : * : * : * : : : : : : : : : : : : : : : : *		
hCLASP4	TPVGFAWVPLLKDGRITFEQQLPVSANLPPGYLNLNDAESRRQCNVDIKWVDGAKPLLK		747
hCLASP5	TLLGYSWLPILLNERLOTGSYCLPVALEKLPNYSMHSAEKVPLQNPFIKWAEGHKGVEN		655
hCLASP3	TPVGYTWIPMLQNGRLKTGQFCLPVSLKPPQAYSVLSPEVP---LPGMKWVDNHKGVEN		721
hCLASP2	TQVGYSWLPLLKDGRVVTSEQHIPVSANLPSGHLGYQELGMGRHYGPEIKWVDGGKPLLK		740
hCLASP7	TPVGFTWIPLLQHGRRLRTGPFCLPVSDQPPPSYSVLTDPVA---LPGMRWVDGHKGVS		708
hCLASP1	TSVGYAWLPLMKHDQIASQEYNIPIATSLPPNYLSFQDSASGKHGGSDIKWVDGGKPLFK		838
	* : : : : : : : . : : : : * : : : : : : : : : : : : : : : : *		



hCLASP4	FKSHLESTIYTQDLHVHKFFHHCQLIQS-----GSKEVPGELIKYLKCLHAM	794
hCLASP5	IEVQAVSSVHTQDNHLEKFFTLCHSLESQVTFPIRVLDQKISEMALEHELKLSIICLNSS	715
hCLASP3	VEVVAVSSIHTQDPYLDKFFALVNALDEH-LFPVRIGDMRIMENNLLENELKSSISALNSS	780
hCLASP2	ISTHLVSTVYTQDQHLHNFQYCKTES-----GAQALGNELVKYLKSLHAM	787
hCLASP7	VELTAVSSVHPQDPYLDKFFTLVHVLEEG-AFPFRLKDTVLEGNVEQELRASLAALRLA	767
hCLASP1	VSTFVVSTVNTQDPHVNAFFQECQKREK-----MSQSPTS NFIRSCKNLLNVE	887
	.. *:: ** ::. ** :	.. *
hCLASP4	EQVMIQFLPVILMQLER-----VLTNMT-----EDDVP	824
hCLASP5	RLEPLVLFHLVLDKLFQLSVQPMVIAGQTANFSQFASFESVVAIANSLHNSKDLSDQHG	775
hCLASP3	QLEPVVRFLHLLDKLILLVIRPPVIAGQIVNLGQASFEAMASIINRLHKNLEGNHDQHG	840
hCLASP2	EGHVMIAFLPTILNQLER-----VLT-RAT-----QEEVA	816
hCLASP7	SPEPLVAFSHHVLDKLVRLVIRPPIISGQIVNLGRGAFEAMAHVVS LVHRSLEAAQDARG	827
hCLASP1	KIHAIMSFLPIILNQLER-----VLVQNE-----EDEIT	916
	. :: * : * : *	: ..
hCLASP4	INCTMV-LLHIVSKCHEEGLDS-----YLRSFIKYS-----FRPEKP	860
hCLASP5	RNCLLASVYHVFRLEPEVQORDVPKSGAPTALLDPRSHTYGRTSAAAVSSKLLQARVMSS	835
hCLASP3	RNSLLASYIHVFRLEPNTYPNSSSPG-PGGLGGSVHYATMARSAVRPASLNLNRSRSLN	899
hCLASP2	VNVTRV-IIHVVAQCHEEGLES-----HLRSYVKYA-----YKAEPY	852
hCLASP7	HCPQLAAYVHYAFRLPGTEPSLPDGAPP----VTVQAATLARGSGRPASLYLARSKSISS	883
hCLASP1	TTVTRV-LPDIVAKCHEEQLDH-----SVQSYIKFV-----FKTRAC	952
	. . . :	:
hCLASP4	SAPQAQLIH-----ETLATTMIAILKQS-----	883
hCLASP5	SNPDLAGTHSAADEEVKNIMSSKIADRNC SRMSYYCSGSSDAPSSPA-----	882
hCLASP3	SNPDISGTPSTPDDEVRSIIGSKGLDRSNSWVNTGGPKAAPWGSNPSPSAESTQAMDRSC	959
hCLASP2	VASEYKTVH-----EELTKSMTTILKPS-----	875
hCLASP7	SNPDLAVAPGSVDDEVSRILASKLLHEELA-LQ-----	915
hCLASP1	KE---RPVH-----EDLAKNVTGLLKSN-----	972
	: . .	
hCLASP4	-----ADFLSINKLLKYS-----WFFFEIIAKSM	907
hCLASP5	-----APRPASKKHFEELALQ-----MVVSTGMVKSM	910
hCLASP3	NRMSSHTETSSFLQTLTGRLPTKKLFHEELALQWVVC SGSVRESALQOAWFFFEIMVKSM	1019
hCLASP2	-----ADFLTSNKLLRYS-----WFFFDVLIKSM	899
hCLASP7	-----WVSSSAVREAILQHA-----WFFFQLMVKSM	942
hCLASP1	-----DSPTVKHVLKHS-----WFFFAIILKSM	995
	. * .. : ***	
Cadherin Cleavage		
hCLASP4	ATYLLEENKIKLRGQRFPEYHHVLHSLLLAIIPHV TIRYAEIPDE---SRNVNYSLAS	964
hCLASP5	AQHVNMDKRDSERRTRFSRDMDDITTIVNVVTSEIAALLVKPQKENEQA EKMNISLAF	970
hCLASP3	VHHLYFNDKLEAERKSREFPERFMD DIAALVSTIASDIVSRFQKDTM---VERLNTSLAF	1076
hCLASP2	AQH LIENSKVKLIRNQRFPASYHHAETVVNMLMPHITQKFGDNPEA---SKNANHSLAV	956
hCLASP7	ALHLLLGQRLDTERKLRFPGRFLDDIT ALVGSVGLVITRVHKDVEL---AEHLNASLAF	999
hCLASP1	AQHLIDTNKIQLERPQRFPESYQNELDNLMVLS DHVIWKYKDALEE---TRRATHSVAR	1052
	. :: . : . * * . : . : : . . . . . * : *	
hCLASP4	FLKRCLTLMDRGFIENLINDYISGFSPKDP-----KVLAEYKFEFLQ TICNHEHYIPLNL	1019
hCLASP5	FLYDLLSLMDRGFVFNLRHYCSQLSAKLSNL---PTLISMRLFLRILCSHEHYLNLNL	1027
hCLASP3	FLNDLLSVMDRGFVFSLIKSCYKQVSSKLYSLPNPSVLVSLRLD FLRIICSHEHYVTNL	1136
hCLASP2	FIKR CFTFMDRGFVFKQINNYISCFAPGDP-----KTLFEYKFEFLRVVCNHEHYIPLNL	1011
hCLASP7	FLSDLLSLVDRGFVFSLVRAHYKQVATRLQSSPNPAALLTLRMEFTRILCSHEHYVTNL	1059
hCLASP1	FLKR CFTFMDRGCVFKMVNNYISMFSGDL-----KTLCOYKFDFLQEVCOHEHFIPCL	1107
	*: : : : * * : . . . . . * : : : * : : * . * * : * *	

FIG. 8  
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## Cadherin EC motif

hCLASP4	PMAFAKPKLQR-----VQDS--NLEYSLSDEYCKHHFLVGI	LLRETSI	1060
hCLASP5	FFMNADTAPTSP--CPSISSQNSSSCSSSQDQKIASMFDLTSEYRQQHFLTGL	LFTELAA	1085
hCLASP3	PCSLTTPPASPSPSVSSATSQSSGFSTNVQDQKIANMFELSVPFQQHYLAGI	VLTELAV	1196
hCLASP2	PMPFGKGRIQR-----YQDL--QLDYSLTDEFRCRNFHFLVGI	LLREVGT	1052
hCLASP7	PCCPLSPPASPSPSVSSTTSQSSTFSSQAPDPKVTSMFELSGPFRQQHFLAGI	LLTELAL	1119
hCLASP1	PIRSANIPDPLTP-----SES----TQELHASDMPEYSVTNEFCRKHFLIGI	LLREVGF	1157
		.... : : : * * * * *	
hCLASP4	ALQDN----YEIRYTAISVIKNLLIKHAFDTRYQHKNQQAQIAQLYLPFVGLLEN	IORL	1116
hCLASP5	ALDAEGEGISKVQRKAVSAIHSLLSSHDLDPRCVKPEVKVKIAALYLPLVGI	ILDALP--	1143
hCLASP3	ILDPDAEGLFGLHKKVINMVHNLSSHDSDPRYSDPQIKARVAMLYLPLIGI	IMETVP--	1254
hCLASP2	ALQEFR----EVRLIAISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGL	LIENVORI	1108
hCLASP7	ALEPEAEGAFILHKKAISAVHSLLCGHDTDPRYAEATVKARVAELYLPLLSI	ARDTLP--	1177
hCLASP1	ALQEDQ----DVRHLALAVLKNLMAKHSFDDRYREPRKQAQIASLYMPPLY	GMLLDNMPRI	1213
	* :	: : : : * * * * * : : : : *	
hCLASP4	AGRDTLYSCA-----AMPN-S-----ASRDEFPCGFTSPANRGSLS	TDKDTAYGS	1160
hCLASP5	-----QL-----	CDFTVADTRRYRTSGSD	1162
hCLASP3	-----QLY-----	DFTETHNQGRPICIA	1276
hCLASP2	NVRDVSPFPVNAGMTVKDESALPA-VNPLVTPQKGSTLDNSLHKDLLGAIS	GIASPYTT	1167
hCLASP7	-----RLH-----	DFAEGPGQRSRLASML	1201
hCLASP1	YDKDLYPFTVNTSNQGSRDDLSNNGGFQSQTAIKHANSVDTSF	SKDVLNSIAAFSSIAIS	1273
		.	
hCLASP4	FQ-NGHGIKREDSRGS LIPEGATGFPDQNTGEN-----	TROSSTRSSVSQYNRLDQYE	1213
hCLASP5	-----EEQEGAGAINQNVALAIAGNNFNLT-----	SGIVLSSLPYKQYNMLNADT	1208
hCLASP3	-----YESESGSMISQTVAMAIAGTSVPQLTR----	PGSFLTSTSGRQHTTFS	1324
hCLASP2	STPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQQSSTLGNS	VVRCDKLDQSE	1227
hCLASP7	-----GEGDIAGTINPSVAMAIAGGPLAPGSR----	ASISQGPPTASRAGCAL	1249
hCLASP1	-----TVNHADSRASLASLDSNPSTNEKSSEKTDNCEKI	PRPLALIGSTLRFDRLDQAE	1327
	.	:	
hCLASP4	IRSLLMCYLYIVKMISEDTLLTYWNKVSPQELINILILLEVCLFHFRYM	GKRNIARVHDA	1273
hCLASP5	TRNLMICFLWIMKNADQSLIRKWIADLPSTQLNRILDLLFICVLCFEYK	GKQSSDKVSTQ	1268
hCLASP3	SRSLICLLWVLKNADETVLQKWFTDLSVLQLNRLLDLLYLCVSCFEYK	GKKVFERMNSL	1384
hCLASP2	IKSLLMCFLYILKSMSDDALFTYWNKASTSEIMDFFTISEVCLHQFQY	MGKRYIARNQEG	1287
hCLASP7	SRTLLACVLWVLKNTTEPALLQRWATDLTLPQLGRLLDLLYLCLAAFEY	GKKAFERINSL	1309
hCLASP1	TRSLLMCFHIMKTISYETLIAYWQRAPSPEVSDFFSILDVCLQNFY	LGKRNIIRKIAA	1387
	: : * * : * . : : : : : : : * * * * :		
hCLASP4	WLSKHFGIDR-----KSQTMPALNRNSGVMQARLOHLSSLESS	-----	1311
hCLASP5	VLQKSRDVKAR-----LEEALLRGEARGEMMRRRAPGNDRFPGLNEN	---	1311
hCLASP3	TFKKS KDMRAK-----LEEAILGSIGARQEMVRRSRGQLERS	PSGSAFGSQ	1430
hCLASP2	LGPIVHDRKS-----QTLPVSRNRTGMMHARLQQLGSLDNS	-----	1323
hCLASP7	TFKKS LDMKAR-----LEEAILGTIGARQEMVRRSRERS	PFGNPEN	1350
hCLASP1	AFKFVQSTQNNGT LKGSNPSCQTSGLLAQWMHSTSRHEGHKQHR	SQTLPIIRGKN	1442
	.	:	
hCLASP4	-----FTLNHSSTTTEADIFHQALLEGNTATEVSLTVLDTISFFT	QCFTQLL	1359
hCLASP5	--LRWKKEQTHWRQANEKLDKTKAEILDQEALISGNLATEAHLI	ILDMQENIQASS-ALD	1368
hCLASP3	ENLRWRKDMTHWRQNTTEKLDKSRAEIEHEALIDGNLATEANLI	ILDTLEIVQTVS-VTE	1489
hCLASP2	-----LTFNHSYGHSDADV LHQS LLEANIATEVCLTALD	TLSLFTLAFKNQLL	1371
hCLASP7	--VRWRKSVTHWKQTS DRVDKTKDEMEHEALVEGNLATEAS	LVVLDTLEIIVQTM-LSE	1407
hCLASP1	--ALSNPKLLQMLDNTMTSNEIDIVHHVDTEANIATEGCLT	ILDVSLFTQTHQRQLQ	1500
	.	:	
		: : . * * * * * . . .	

hCLASP4 NNDGHNPLMKKVFDIHLAFLKNGQSEVSLKHVFASLRAFISKFPSAFFKGRVNMCAAFCY 1419
hCLASP5 CKDS---LLGGVLRVLVNSLNCDSQSTTYLTHCFATLRALIAKFGDLLFEEVEQC FDLCH 1425
hCLASP3 SKES---ILGGVLKVLHSMACNQSAVYLQHC FATORALVSKFPELLFEEETE QCADLCL 1546
hCLASP2 ADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRS LIYKFPSTFYEGRADMCAALCY 1431
hCLASP7 ARE---VLGAVLKVVLYSLGSAQSALFLOHGLATQALVSKFPELLFEEDTELCADLCL 1464
hCLASP1 QCDCQNSLMKRGFDTYMLFFQVNQSATA LKHVFASLRLFVCKFPSAFFQGPADLCGSFCY 1560
...
hCLASP4 EVLKCCTSKISSTRNEASALLYLLMRNNFEYTKRKTFLRTHLQII IAVS QLIADVALSGG 1479
hCLASP5 QVLHHCSSSMDVTRSQCACATLYLLMR--FSFGATSNFARVKMQVTMSLASLVGRAPDFNE 1483
hCLASP3 RLLRHCS SIGTIRSHPSASLYLLMR--QNFEIGNNFARVKMQVPMSLSSLVGTSQNFNE 1604
hCLASP2 EILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTHLQVIISVS QLIADVVGIGE 1491
hCLASP7 RLLRHCGSRISTIRTHASASLYLLMR--QNFEIGHNFARVKMQVTMSLSSLVGTTQNFSE 1522
hCLASP1 EVLKC CNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSHLQLIKAVS QLIADAG-IGG 1619
...
hCLASP4 SRFOESLFI INNFANS DRPMKATAFPAEVKDLTKRIRTVLMATAQ MKEHEKDP EMLIDLQ 1539
hCLASP5 EHLRRSLRTILAYSEEDTAMQMTFPPTQVEELLCNLNSILYDTVKMREFQEDPEMLMDLM 1543
hCLASP3 EFLRRSLKTILTYAEEDLELRETTFPDQVQDLVFNLMILSDTVKMKEHQEDPEMLIDL M 1664
hCLASP2 TRFQQSLSI INNCANS DRLIKHTSFSSDVKDLTKRIRTVLMATAQ MKEHENDPEMLVDLQ 1551
hCLASP7 EHLRRSLKTILTYAEEDMGLRDSTFAEQVQDLMFNLMILTDTVKMKEHQEDPEMLIDL M 1582
hCLASP1 SRFQHSLAITNNFANGDKQMKNSNFP AEVKDLTKRIRTVLMATAQ MKEHEKDP EMLVDLQ 1679
...
transmembrane
hCLASP4 YSLAKSYASTPELRKTWLD SMAKIHVKNGD FSEAAMCYVHVAALVAEFLHRKK----- 1592
hCLASP5 YRIAKSYQASPDRLTLWLQNM AEKHTKKKCYTEAAMCLVHAAALVAEYLSMLEDH----- 1598
hCLASP3 YRIAKGYQTSPE-RLTWLQNMAGKHSERSNHAEAAQCLVHSAALVAEYLSMLED R----- 1718
hCLASP2 YSLAKSYASTPELRKTWLD SMARIHVKNGLSEAAMCYVHV TALVAEYLTRKG----- 1604
hCLASP7 YRIARGYQGPSDLRLTLWLQNMAGKHAELGNHAEAAQCMVHAAALVAEYI ALLEDQ----- 1637
hCLASP1 YSLANSYASTPELRRTWLESMAKIHARNGD LSEAAMCYIHIAALIAEYIKRKG YWKVEKI 1739
...
hCLASP4 -----LFPNGCSAFKKITPNIDE EGAMKEDAGMMD----- 1622
hCLASP5 -----SYLPVGSVSFQNISSNVLEESVSEDTLSPDEDGV 1633
hCLASP3 -----KYLPGCVTFQNISSNVLEESAVSDDVSPDEEGI 1753
hCLASP2 -----VFRQGCTAFRVITPNIDE EASM MEDVGMQD----- 1634
hCLASP7 -----RHLPGCVSFQNISSNVLEESAISDDILSPDEEGF 1672
hCLASP1 CTASLLSEDTHPCDSNSLLTTPSGGSMFSGWPAFLSITPNIKEEGA AKEDSGMHD----- 1795
...
ITAM
hCLASP4 ---VHYSEEV LLELLEQCVDGLWKAERYEII SEISK LIVPIYEKRREFEKL TQVYRTI HG 1679
hCLASP5 CAGQYFTESGLVGLLEQA AELFSTGGLYETVNEVYKLVIP ILEAHREFRKL TLTHSKLQR 1693
hCLASP3 CSGKYFTESGLVGLLEQA AASF SMAGMYEAVNEVYKVLIP IHEANRDAKKLSTIHGKLQE 1813
hCLASP2 ---VHFNE DVLME LLEQCADGLWKAERYELIADIYKLI IPIYEKRR----- 1677
hCLASP7 CSGKHFTELGLVGLLEQA AGYFTMGGLYEAVNEVYKNLIP ILEAHRDYKKLA AVHGKLQE 1732
hCLASP1 ---TPYNENILVEQLYMCGEFLWKSERYELIADV NKP IIAVF EKQRDFKKLS DLYYDIHR 1852
...
ITAM DOCK motif DOCK motif ITAM
hCLASP4 AYTKI LEVMHTKKRLLGTFFRVA FYGQSFFEEEDGKEYIYKEKLTGLSEISLR LVKIYG 1739
hCLASP5 AFDSI VNKD H--KRMFGTYFRVGF FG-SKFGDLDEQE FVYKEFAITKLPEISHRLEAFYG 1750
hCLASP3 AFSKI VHQSTGWERMFGTYFRVGF FG-TKFGDLDEQE FVYKEFAITKLAEISHRLEGFYG 1872
hCLASP2 -----DFFEDEDGKEYIYKEKLTPLSEISQRLLK IYS 1710
hCLASP7 AFTKIMHQSSGWERVFGTYFRVGF FG-AHFGDLDEQE FVYKEFSITKLAEISHRLEE FYT 1791
hCLASP1 SYLKVAEVVNSEKRLFGRYYRVA FYGQGFEEEGKEYIYKEKLTGLSEISQRLLK IYA 1912
...

FIG. 8
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	ITAM	ITAM	
hCLASP4	EKFGTENVKIIQSDSKVNAKELDPHYAHIQVTYVKEHYFDDKELTERKTEFERNHNISRFEV	1799	
hCLASP5	QCFGAEFVEVIKdstpVDKTKLDPNKAYIQITFVEBYFDEYEMKDRVTYFEKNFNLRRFM	1810	
hCLASP3	ERFGEDVVEVIKDSNPVDKCKLDPNKAYIQITFVEBYFDTYEMKDRITYFDKNYNLRRFM	1932	
hCLASP2	DKFGSENVKMIQDSGKVNPKDLDSKYAYIQVTHVIEFFDEKELQERKTEFERSHNIRRFM	1770	
hCLASP7	ERFGDDVVEIIKDSYPVDKSKLDSQKAYIQITFVEBYFDTYELKDRVTYFDRNYGLRTFL	1851	
hCLASP1	DKFGADNVKIIQDSNKNVNPKDLDPHYAYIQVTYVTEFFEEKEIEDRKTDfEMHHNINRFV	1972	
	: ** : *::*:** * : .***: *::*:** * : *:: * : * * : . . : * :		
	ITAM	DOCK motif	
hCLASP4	FEAPYTLGKKQGCIEEQCKRRTILTTSNSFPYVKKRIPINCEQQINLKPIDGATDEIKD	1859	
hCLASP5	YTTPFTLEGRPRGELHEQYRRNTVLTTHAFHYIKTRISVIOKEEFVLTPIEVAIEDMKK	1870	
hCLASP3	YCTPFTLDGRAHGEHQFKRKTILTTSNHFHYIKTRVNVTHKEEILTPIEVAIEDMQK	1992	
hCLASP2	FEMPFTQTGKRQGGVEEQCKRRTILTAIHCFHYVKKRIPVMYQHHTDLNPIEVAIDEMSK	1830	
hCLASP7	FCTPFTPDGRAHGEHQHKKRKTLLSTDHAFHYIKTRIRVCHREETVLTPEVAIEDMQK	1911	
hCLASP1	FETPFTLSGKKHGGVAEQCKRRTILTTSNLFHYVKKRIQVISQSSTELNPIEVAIDEMSR	2032	
	: *:* * : * : * : * : * : * : * : * : * : * : * : * : * : * : *		
	Coiled-coil		
hCLASP4	KTAELOKLCSSSTDVDMIQLQLKLOQWVSVQVNAGPLAYARAFLNDSQASKYPPKKVSELK	1919	
hCLASP5	KTLLQAVAINQEPDAKMLQMVLOQSVGATVNQGPLEVAQVFLAEIPADPKLYRHNNKLR	1930	
hCLASP3	KTQELAFATHQDPADPKMLQMVLOQSVGTTVNQGPLEVAQVFLSEIPSDPKLFRHHNNKLR	2052	
hCLASP2	KVAELRQLCSSAEVDMIKLQLKLOQSVSVQVNAGPLAYARAFLLDTNTKRYPDNKVKLLK	1890	
hCLASP7	KTRELAFAEQDPPDAKMLQMVLOQSVGPTVNQGPLEVAQVFLAEIPEDPKLFRHHNNKLR	1971	
hCLASP1	KVSELNQLCTMEEVDMISLQLKLOQSVSVKVNAGPMAYARAFLEETNAKKYPDNQVKLLK	2092	
	*. : * * : * : * : * : * : * : * : * : * : * : * : * : * : * : *		
	Coiled-coil		
hCLASP4	DMFRKFIQACSALELNERLIKEDQVEYHEGLKSNFRDMVKELSDIIEHQILQEDTMHSP	1979	
hCLASP5	LCFKEFIMRCGRAVEKNKRLITADQREYQOELKKNYNKLKENLRPMIERKIPELYKPIFR	1990	
hCLASP3	LCFKDFTKRCEALRKNKSLIGPVQKEYQRELGKLSSP-----	2090	
hCLASP2	EVFRQFVEACGOALAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQICPLEEKTS-	1949	
hCLASP7	LCFKDFCKKCEALRKNKALIGPDQKEYHRELEARNYCRLEALQPIILTQRLPQLMAPTP-	2030	
hCLASP1	EIFRQFADACGOALDVNERLIKEDQLEYQEELRSHYKMDLSELSTVMNEQITGRDDLSKR	2152	
	*.: * * : * : * : * : * : * : * : * : * : * : * : * : * : * : *		
	PDZ ligand		
hCLASP4	WMSNTLHVFCASISGTSSDRGYGSPHYAEV--	2008	
hCLASP5	VESQKRDSFHRSSFRCETQLSQGS-----	2015	
hCLASP3	-----		
hCLASP2	VLPNSLHIFNAISGTPTSTMVHGMSSTSSVV	1980	
hCLASP7	--PGLRNSLNRASFRKADL-----	2047	
hCLASP1	GVDQTCSTRVISKATPALPTVSISSAEV--	2180	

FIG. 8  
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